

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 17, 2002, 16:30:06 ; Search time 326.88 Seconds
(without alignments)
10583.647 Million cell updates/sec

Title: US-10-007-010-3

Perfect score: 2015

Sequence: 1 cggaggcacggaagtggg.....atataaatgcaagcttcaag 2015

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2057840

Minimum DB seq length: 0

Maximum DB seq length: 105

Post-processing: Listing first 65 summaries

Database : N_Geneseq_032802.*

1: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
2: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SID55/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SID55/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SID55/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SID55/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SID55/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	1.5	31	22	AAI30734
2	31	1.5	31	22	AAI30735
3	31	1.5	31	22	AAI30736
4	31	1.5	31	22	AAI30737
5	31	1.5	31	22	AAI30738
c 6	27	1.3	33	22	AAH41498
7	26	1.3	32	22	AAH41491
c 8	26	1.3	32	22	AAH41492
c 9	25	1.2	32	22	AAH41501

10	25	1.2	51	23	ABL00375	Human silent nonco
11	24	1.2	32	22	AAH41500	Human tyrosine kin
12	24	1.2	78	22	AAC90044	PCR primer used to
13	21	1.0	21	22	AAF55624	Human gene single
14	21	1.0	21	22	AAF55625	Human gene single
15	21	1.0	21	22	AAF55626	Human gene single
16	21	1.0	21	22	AAF55627	Human gene single
17	21	1.0	21	22	AAF55628	Human gene single
18	21	1.0	21	22	AAF55629	Human gene single
19	21	1.0	21	22	AAF55630	Human gene single
20	20	1.0	20	16	AAH41207	Human gene signatu
c 21	20	1.0	20	16	AAH41208	Human gene signatu
c 22	19	0.9	51	22	AAH33024	Human SNP oligonuc
c 23	19	0.9	51	22	AAH33025	Human SNP oligonuc
24	18	0.9	19	21	AAH82879	cdk4 ribozyme bind
25	18	0.9	19	21	AAH82879	Cell-cycle depende
26	18	0.9	19	22	AAH58041	Chemically modifie
27	18	0.9	20	20	AAH29331	JNK2-specific prob
c 28	18	0.9	20	21	AAC62874	JNK antisense olig
c 29	18	0.9	20	21	AAC62885	JNK antisense olig
c 30	18	0.9	20	21	AAH48651	Antisense oligonuc
c 31	18	0.9	20	22	AAH23754	JNK1 antisense oli
c 32	18	0.9	20	22	AAH99183	Immunostimulatory
33	18	0.9	34	22	AAH41497	Human tyrosine kin
34	17	0.8	19	21	AAH82878	cdk4 ribozyme bind
35	17	0.8	19	22	AAH58040	Cell-cycle depende
c 36	17	0.8	20	20	AAH01356	PCR primer for you
c 37	17	0.8	20	22	AAH72970	Human daxx inhibit
c 38	17	0.8	23	14	AAQ49744	PTK primer pTK2.
c 39	17	0.8	23	16	AAH03086	Protein tyrosine-k
40	17	0.8	25	21	AAH37264	PCR primer for SGR
c 41	17	0.8	57	22	AAH04769	Synthetic gene-shg
42	16	0.8	18	22	AAH62905	Shrimp white spot
43	16	0.8	20	20	AAH03686	PCR primer used to
c 44	16	0.8	20	20	AAH79186	Human aggrecan amp
45	16	0.8	22	19	AAC69364	Human ABC1 gene in
c 46	16	0.8	64	21	AAH19448	Oligonucleotide #4
c 47	16	0.8	75	22	AAH72971	Human foetal liver
c 48	16	0.8	75	22	ABA38521	Probe #16987 for g
c 49	16	0.8	75	22	AAH21402	Human brain expres
c 50	16	0.8	75	22	AAH47563	Human bone marrow
c 51	16	0.8	75	22	AAH25979	Probe #15912 for g
c 52	16	0.8	75	22	AAH53395	Probe #22081 used
53	16	0.8	90	22	AAH44421	Human bone marrow
54	16	0.8	90	22	AAH50415	Probe #19101 used
c 55	16	0.8	98	22	ABA51445	Human breast cell
c 56	16	0.8	98	22	ABA69473	Human foetal liver
c 57	16	0.8	98	22	ABA36398	Probe #14864 for g
c 58	16	0.8	98	22	AAH17738	Human brain expres
c 59	16	0.8	98	22	AAH43549	Human bone marrow
c 60	16	0.8	98	22	AAH24335	Probe #14268 for g
c 61	16	0.8	98	22	AAH49605	Probe #18291 used
c 62	16	0.8	98	22	AAH09877	Probe #9868 used t
c 63	16	0.8	101	22	AAH50492	Insulin receptor m
64	16	0.8	101	22	AAH31189	Human insulin rece
65	16	0.8	101	22	AAH31286	Human insulin rece

ALIGNMENTS

RESULT 1	AAI30734	standard; DNA; 31 BP.
ID	AAI30734	
XX	AAI30734;	
AC	AAI30734;	
DT	18-OCT-2001	(first entry)
XX	Human single nucleotide polymorphism (SNP) HCK 1.	
DE	Human; resequence; genotype; disease; forensic; paternity testing;	
XX	single nucleotide polymorphism; SNP; ss.	
KW		

```
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Variation replace(16,T)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
XX PN WO200166800-A2.
XX
XX PD 13-SEP-2001.
XX
XX PF 07-MAR-2001; 2001WO-US07268.
XX
XX PR 07-MAR-2000; 2000US-0187510.
XX
XX PR 22-MAY-2000; 2000US-0206129.
XX
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
XX PI Cargill M, Ireland JS, Lander ES;
XX
XX DR WPI; 2001-522952/57.
XX
XX PT Nucleic acid molecules from the human genome which include polymorphic
FT sites, useful in methods for predicting the presence, absence or
FT severity of a particular phenotype or disorder (e.g. diabetes)
FT associated with a particular genotype -
XX
XX PS- Claim 1; Page 104; 145pp; English.
XX
XX CC The invention relates to the identification of nucleic acid molecules
CC (AAI29513-AAI31314) from the human genome which include polymorphic sites
CC which can predispose individuals to disease. Various genes from a number
CC of individuals were resequenced and single nucleotide polymorphisms
CC (SNPs) in these genes discovered. The method is useful for predicting the
CC presence, absence or severity of a particular phenotype or disorder (e.g.
CC diabetes) associated with a particular genotype. The nucleic acids
CC containing the polymorphic sites may be useful in forensics and paternity
CC testing.
XX
XX SQ Sequence 31 BP; 10 A; 9 C; 7 G; 5 T; 0 other;
XX
XX
XX Query Match 1.5%; Score 31; DB 22; Length 31;
XX Best Local Similarity 100.0%; Pred. No. 7.6e-05;
XX Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1152 gggcagcaagcagcattgccaaactcatt 1182
XX ||||||||||||||||||||||||||||
XX Db 1 gggcagcaagcagcattgccaaactcatt 31
XX
XX RESULT 2
XX AAI30735
XX ID AAI30735 standard; DNA; 31 BP.
XX
XX AC AAI30735;
XX
XX DT 18-OCT-2001 (first entry)
XX
XX DE Human single nucleotide polymorphism (SNP) HCK 2.
XX
XX KW Human; resequence; genotype; disease; forensic; paternity testing;
XX KW single nucleotide polymorphism; SNP; ss.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Variation replace(16,T)
XX FT /*tag= a
XX FT /standard_name= "single nucleotide polymorphism"
XX
XX PN WO200166800-A2.
```

```
XX
XX PD 13-SEP-2001.
XX
XX PF 07-MAR-2001; 2001WO-US07268.
XX
XX PR 07-MAR-2000; 2000US-0187510.
XX
XX PR 22-MAY-2000; 2000US-0206129.
XX
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
XX PI Cargill M, Ireland JS, Lander ES;
XX
XX DR WPI; 2001-522952/57.
XX
XX PT Nucleic acid molecules from the human genome which include polymorphic
FT sites, useful in methods for predicting the presence, absence or
FT severity of a particular phenotype or disorder (e.g. diabetes)
FT associated with a particular genotype -
XX
XX PS Claim 1; Page 104; 145pp; English.
XX
XX CC The invention relates to the identification of nucleic acid molecules
CC (AAI29513-AAI31314) from the human genome which include polymorphic sites
CC which can predispose individuals to disease. Various genes from a number
CC of individuals were resequenced and single nucleotide polymorphisms
CC (SNPs) in these genes discovered. The method is useful for predicting the
CC presence, absence or severity of a particular phenotype or disorder (e.g.
CC diabetes) associated with a particular genotype. The nucleic acids
CC containing the polymorphic sites may be useful in forensics and paternity
CC testing.
XX
XX SQ Sequence 31 BP; 8 A; 8 C; 9 G; 6 T; 0 other;
XX
XX
XX Query Match 1.5%; Score 31; DB 22; Length 31;
XX Best Local Similarity 100.0%; Pred. No. 7.6e-05;
XX Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1195 cagattgcagaagcattgcccttcacgcgc 1225
XX ||||||||||||||||||||||||||||
XX Db 1 cagattgcagaagcattgcccttcacgcgc 31
XX
XX RESULT 3
XX AAI30736
XX ID AAI30736 standard; DNA; 31 BP.
XX
XX AC AAI30736;
XX
XX DT 18-OCT-2001 (first entry)
XX
XX DE Human single nucleotide polymorphism (SNP) HCK 3.
XX
XX KW Human; resequence; genotype; disease; forensic; paternity testing;
XX KW single nucleotide polymorphism; SNP; ss.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Variation replace(16,A)
XX FT /*tag= a
XX FT /standard_name= "single nucleotide polymorphism"
XX
XX PN WO200166800-A2.
XX
XX PD 13-SEP-2001.
XX
XX PF 07-MAR-2001; 2001WO-US07268.
XX
XX PR 07-MAR-2000; 2000US-0187510.
XX
XX PR 22-MAY-2000; 2000US-0206129.
XX
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
```

```
XX PI Cargill M, Ireland JS, Lander ES;
XX DR WPI; 2001-522952/57.
XX CC Nucleic acid molecules from the human genome which include polymorphic
PT sites, useful in methods for predicting the presence, absence or
PT severity of a particular phenotype or disorder (e.g. diabetes)
PT associated with a particular genotype -
XX CC
XX PS Claim 1; Page 104; 145pp; English.
XX CC
XX CC The invention relates to the identification of nucleic acid molecules
CC (AAI29513-AAI31314) from the human genome which include polymorphic sites
CC which can predispose individuals to disease. Various genes from a number
CC of individuals were resequenced and single nucleotide polymorphisms
CC (SNPs) in these genes discovered. The method is useful for predicting the
CC presence, absence or severity of a particular phenotype or disorder (e.g.
CC diabetes) associated with a particular genotype. The nucleic acids
CC containing the polymorphic sites may be useful in forensics and paternity
CC testing.
XX SQ Sequence 31 BP; 6 A; 9 C; 6 G; 10 T; 0 other;

Query Match 1.5%; Score 31; DB 22; Length 31;
Best Local Similarity 100.0%; Pred. No. 7.6e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1405 ttaccatcaagtcagacgtctgtgctcttg 1435
Db 1 ttaccatcaagtcagacgtctgtgctcttg 31

RESULT 4
AAI30737
ID AAI30737 standard; DNA; 31 BP.
XX AC AAI30737;
XX DT 18-OCT-2001 (first entry)
XX DE Human single nucleotide polymorphism (SNP) HCK 4.
XX KW Human; resequence; genotype; disease; forensic; paternity testing;
XX KW single nucleotide polymorphism; SNP; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Variation replace(16,A)
XX FT /*tag= a
XX FT /standard_name= "single nucleotide polymorphism"
XX PN WO200166800-A2.
XX PD 13-SEP-2001.
XX PF 07-MAR-2001; 2001WO-US07268.
XX PR 07-MAR-2000; 2000US-0187510.
XX PR 22-MAY-2000; 2000US-0206129.
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX PI Cargill M, Ireland JS, Lander ES;
XX DR WPI; 2001-522952/57.
XX CC Nucleic acid molecules from the human genome which include polymorphic
PT sites, useful in methods for predicting the presence, absence or
PT severity of a particular phenotype or disorder (e.g. diabetes)
PT associated with a particular genotype -
PT
```

```
XX PS Claim 1; Page 104; 145pp; English.
XX CC
XX CC The invention relates to the identification of nucleic acid molecules
CC (AAI29513-AAI31314) from the human genome which include polymorphic sites
CC which can predispose individuals to disease. Various genes from a number
CC of individuals were resequenced and single nucleotide polymorphisms
CC (SNPs) in these genes discovered. The method is useful for predicting the
CC presence, absence or severity of a particular phenotype or disorder (e.g.
CC diabetes) associated with a particular genotype. The nucleic acids
CC containing the polymorphic sites may be useful in forensics and paternity
CC testing.
XX SQ Sequence 31 BP; 7 A; 7 C; 10 G; 7 T; 0 other;

Query Match 1.5%; Score 31; DB 22; Length 31;
Best Local Similarity 100.0%; Pred. No. 7.6e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 921 gtttggggaagtctgtggtggccacctacaac 951
Db 1 gtttggggaagtctgtggtggccacctacaac 31

RESULT 5
AAI30738
ID AAI30738 standard; DNA; 31 BP.
XX AC AAI30738;
XX DT 18-OCT-2001 (first entry)
XX DE Human single nucleotide polymorphism (SNP) HCK 5.
XX KW Human; resequence; genotype; disease; forensic; paternity testing;
XX KW single nucleotide polymorphism; SNP; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Variation replace(16,G)
XX FT /*tag= a
XX FT /standard_name= "single nucleotide polymorphism"
XX PN WO200166800-A2.
XX PD 13-SEP-2001.
XX PF 07-MAR-2001; 2001WO-US07268.
XX PR 07-MAR-2000; 2000US-0187510.
XX PR 22-MAY-2000; 2000US-0206129.
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX PI Cargill M, Ireland JS, Lander ES;
XX DR WPI; 2001-522952/57.
XX CC Nucleic acid molecules from the human genome which include polymorphic
PT sites, useful in methods for predicting the presence, absence or
PT severity of a particular phenotype or disorder (e.g. diabetes)
PT associated with a particular genotype -
XX CC
XX PS Claim 1; Page 104; 145pp; English.
XX CC
XX CC The invention relates to the identification of nucleic acid molecules
CC (AAI29513-AAI31314) from the human genome which include polymorphic sites
CC which can predispose individuals to disease. Various genes from a number
CC of individuals were resequenced and single nucleotide polymorphisms
CC (SNPs) in these genes discovered. The method is useful for predicting the
CC presence, absence or severity of a particular phenotype or disorder (e.g.
CC diabetes) associated with a particular genotype. The method is useful for predicting the
CC presence, absence or severity of a particular phenotype or disorder (e.g.
```

CC diabetes) associated with a particular genotype. The nucleic acids
 CC containing the polymorphic sites may be useful in forensics and paternity
 CC testing.

XX
 SQ Sequence 31 BP; 12 A; 11 C; 5 G; 3 T; 0 other;

Query Match 1.5%; Score 31; DB 22; Length 31;
 Best Local Similarity 100.0%; Pred. No. 7.6e-05;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 aaaaactgaaccagcgcagccacactgt 249
 |||||
 Db 1 aaaaactgaaccagcgcagccacactgt 31

RESULT 6
 AAH41498/C
 ID AAH41498 standard; DNA; 33 BP.

XX AAH41498;

XX 23-AUG-2001 (first entry)

XX Human tyrosine kinase Hck PCR primer SEQ ID NO:10.

XX Human; tyrosine kinase Hck binding protein; tyrosine kinase; Hck;
 KW tumour lethal factor; tumour necrosis factor alpha; apoptosis; HSB-1;
 KW Hck signal transduction; human immunodeficiency virus; HIV infection;
 KW anticancer; PCR primer; ss.

XX Homo sapiens.

XX WO200132869-A1.

XX 10-MAY-2001.

XX 26-OCT-2000; 2000WO-JP07500.

XX 29-OCT-1999; 99JP-0309957.

XX (SSSE) SSP CO LTD.

XX Taniyama T, Narita T;

XX WPI; 2001-316440/33.

XX New proteins which bind to human tyrosine kinase Hck for promotion of
 PT apoptosis and for the elucidation of the mechanism of Hck signal
 PT transduction

XX Example 3; Page 33; 45pp; Japanese.

XX The present invention describes a protein, designated HSB-1, which binds
 CC to human tyrosine kinase Hck. Also described are: (1) nucleic acids
 CC encoding the protein and its derivatives; (2) recombinant vectors
 CC containing the nucleic acids; and (3) host cells transformed by the
 CC vectors and expressing the protein. HSB-1 has cytostatic activity, binds
 CC tyrosine kinase, enhances tumour necrosis factor alpha and promotes
 CC apoptosis. HSB-1 proteins are used for the elucidation of the mechanism
 CC of Hck signal transduction and of the role of Hck in human
 CC immunodeficiency virus (HIV) infection. They can be used for the
 CC treatment of infections and other diseases with which Hck is associated.
 CC They promote the anticancer activity of tumour necrosis factor alpha.
 CC The present sequence represents a PCR primer for the human tyrosine
 CC kinase Hck, which is used in an example from the present invention.

XX Sequence 33 BP; 2 A; 8 C; 11 G; 12 T; 0 other;

Query Match 1.3%; Score 27; DB 22; Length 33;
 Best Local Similarity 100.0%; Pred. No. 0.0071;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1657 acagagagccagtaccacacagcagcca 1683
 |||||
 Db 33 ACAGAGAGCCAGTACCACACAGCAGCCA 7

RESULT 7

AAH41491

ID AAH41491 standard; DNA; 32 BP.

XX AAH41491;

XX 23-AUG-2001 (first entry)

XX Human tyrosine kinase Hck binding protein cloning PCR primer SEQ:3.

XX Human; tyrosine kinase Hck binding protein; tyrosine kinase; Hck;
 KW tumour lethal factor; tumour necrosis factor alpha; apoptosis; HSB-1;
 KW Hck signal transduction; human immunodeficiency virus; HIV infection;
 KW anticancer; PCR primer; ss.

XX Homo sapiens.

XX WO200132869-A1.

XX 10-MAY-2001.

XX 26-OCT-2000; 2000WO-JP07500.

XX 29-OCT-1999; 99JP-0309957.

XX (SSSE) SSP CO LTD.

XX Taniyama T, Narita T;

XX WPI; 2001-316440/33.

XX New proteins which bind to human tyrosine kinase Hck for promotion of
 PT apoptosis and for the elucidation of the mechanism of Hck signal
 PT transduction

XX Example 1; Page 30; 45pp; Japanese.

XX The present invention describes a protein, designated HSB-1, which binds
 CC to human tyrosine kinase Hck. Also described are: (1) nucleic acids
 CC encoding the protein and its derivatives; (2) recombinant vectors
 CC containing the nucleic acids; and (3) host cells transformed by the
 CC vectors and expressing the protein. HSB-1 has cytostatic activity, binds
 CC tyrosine kinase, enhances tumour necrosis factor alpha and promotes
 CC apoptosis. HSB-1 proteins are used for the elucidation of the mechanism
 CC of Hck signal transduction and of the role of Hck in human
 CC immunodeficiency virus (HIV) infection. They can be used for the
 CC treatment of infections and other diseases with which Hck is associated.
 CC They promote the anticancer activity of tumour necrosis factor alpha.
 CC The present sequence represents a PCR primer used in the cloning of
 CC HSB-1, which is used in an example from the present invention.

XX Sequence 32 BP; 8 A; 5 C; 9 G; 10 T; 0 other;

Query Match 1.3%; Score 26; DB 22; Length 32;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 350 tcgtgtgtccctgtatgattacgag 375
 |||||
 Db 7 tcgtgtgtccctgtatgattacgag 32

RESULT 8

AAH41492/C

ID AAH41492 standard; DNA; 32 BP.

XX

```

AC AAH41492;
XX
DT 23-AUG-2001 (first entry)
XX
DE Human tyrosine kinase Hck binding protein cloning PCR primer SEQ:4.
XX
KW Human: tyrosine kinase Hck binding protein; tyrosine kinase; Hck;
KW tumour lethal factor; tumour necrosis factor alpha; apoptosis; HSB-1;
KW Hck signal transduction; human immunodeficiency virus; HIV infection;
KW anticancer; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200132869-A1.
XX
PD 10-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-JP07500.
XX
PR 29-OCT-1999; 99JP-0309957.
XX
PA (SSSE ) SSP CO LTD.
XX
PI Taniyama T, Narita T;
XX
DR WPI; 2001-316440/33.
XX
PT New proteins which bind to human tyrosine kinase Hck for promotion of
PT apoptosis and for the elucidation of the mechanism of Hck signal
PT transduction
XX
PS Example 1; Page 31; 45pp; Japanese.
XX
CC The present invention describes a protein, designated HSB-1, which binds
CC to human tyrosine kinase Hck. Also described are: (1) nucleic acids
CC encoding the protein and its derivatives; (2) recombinant vectors
CC containing the nucleic acids; and (3) host cells transformed by the
CC vectors and expressing the protein. HSB-1 has cytostatic activity, binds
CC tyrosine kinase, enhances tumour necrosis factor alpha and promotes
CC apoptosis. HSB-1 proteins are used for the elucidation of the mechanism
CC of Hck signal transduction and of the role of Hck in human
CC immunodeficiency virus (HIV) infection. They can be used for the
CC treatment of infections and other diseases with which Hck is associated.
CC They promote the anticancer activity of tumour necrosis factor alpha.
CC The present sequence represents a PCR primer used in the cloning of
CC HSB-1, which is used in an example from the present invention.
XX
SQ Sequence 32 BP; 7 A; 10 C; 9 G; 6 T; 0 other;

Query Match 1.3%; Score 26; DB 22; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 796 gacgggtctctgccagaaactgtcgg 821
DB 32 GACGGGCTCTGCCAGAACTGTGGT 7

RESULT 9
AAH41501/C
ID AAH41501 standard; DNA; 32 BP.
XX
AC AAH41501;
XX
DT 23-AUG-2001 (first entry)
XX
DE Human tyrosine kinase Hck binding protein cloning PCR primer SEQ:15.
XX
KW Human: tyrosine kinase Hck binding protein; tyrosine kinase; Hck;
KW tumour lethal factor; tumour necrosis factor alpha; apoptosis; HSB-1;
KW Hck signal transduction; human immunodeficiency virus; HIV infection;
KW anticancer; PCR primer; ss.

```

```

XX Homo sapiens.
OS
XX WO200132869-A1.
XX
XX 10-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-JP07500.
XX
XX 29-OCT-1999; 99JP-0309957.
XX
XX (SSSE ) SSP CO LTD.
XX
XX Taniyama T, Narita T;
XX
XX WPI; 2001-316440/33.
XX
XX New proteins which bind to human tyrosine kinase Hck for promotion of
XX apoptosis and for the elucidation of the mechanism of Hck signal
XX transduction
XX
XX Example 4; Page 41; 45pp; Japanese.
XX
CC The present invention describes a protein, designated HSB-1, which binds
CC to human tyrosine kinase Hck. Also described are: (1) nucleic acids
CC encoding the protein and its derivatives; (2) recombinant vectors
CC containing the nucleic acids; and (3) host cells transformed by the
CC vectors and expressing the protein. HSB-1 has cytostatic activity, binds
CC tyrosine kinase, enhances tumour necrosis factor alpha and promotes
CC apoptosis. HSB-1 proteins are used for the elucidation of the mechanism
CC of Hck signal transduction and of the role of Hck in human
CC immunodeficiency virus (HIV) infection. They can be used for the
CC treatment of infections and other diseases with which Hck is associated.
CC They promote the anticancer activity of tumour necrosis factor alpha.
CC The present sequence represents a PCR primer used in the cloning of
CC HSB-1, which is used in an example from the present invention.
XX
XX Sequence 32 BP; 8 A; 9 C; 10 G; 5 T; 0 other;

Query Match 1.2%; Score 25; DB 22; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 505 gccgcgcttgactctctggagacag 529
DB 32 GCCCGCGTGTGACTCTCTGGAGACAG 8

RESULT 10
ABL00375
ID ABL00375 standard; DNA; 51 BP.
XX
XX ABL00375;
XX
XX 05-MAR-2002 (first entry)
XX
XX Human silent noncoding SNP oligonucleotide SEQ ID NO:366.
XX
XX Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
XX immunosuppressive; antinflammatory; neuroprotective; antimicrobial;
XX autoimmune disease; inflammation; cancer; nervous system disease;
XX infection; polymorphic protein; ds.
XX
XX Homo sapiens.
XX
XX WO200138586-A2.
XX
XX 31-MAY-2001.
XX
XX 22-NOV-2000; 2000WO-US32311.
XX
XX 24-NOV-1999; 99US-0167383.
XX
XX

```

```

XX PA (CURA-) CURAGEN CORP.
XX PI Shinkets RA, Leach M;
XX DR WPI; 2001-355949/37.
XX
XX PT Isolated human nucleic acids comprising one or more single nucleotide
XX PT polymorphisms, useful for treating a subject suffering from a
XX PT pathology, e.g. autoimmune diseases, ascribed to the presence of a
XX PT sequence polymorphism -
XX
XX PS Claim 1; Page 359; 674pp; English.
XX
XX CC ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
XX CC comprising one or more single nucleotide polymorphisms (SNPs)...ABB56531
XX CC to ABB56903 represent human peptides encoded by some of the SNP
XX CC oligonucleotides. The sequences from the present invention can have
XX CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
XX CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
XX CC and antibodies from the present invention can be used for treating a
XX CC subject suffering from, at risk for, or suspected of, suffering from a
XX CC pathology ascribed to the presence of a sequence polymorphism. The
XX CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
XX CC the nervous system, and infection by pathogenic microorganisms. The SNPs
XX CC are also useful for determining which forms of a characterised
XX CC polymorphism are present in individuals. The antibodies may be used in
XX CC the detection, quantitation and/or cellular or tissue localisation of a
XX CC polymorphic protein (e.g., for use in measuring levels of the
XX CC polymorphic protein within appropriate physiological samples).
XX
XX SQ Sequence 51 BP; 10 A; 17 C; 13 G; 11 T; 0 other;

Query Match 1.2%; Score 25; DB 23; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 722 ggggcttctacatccccccgaag 746
DB 1 ggggcttctacatccccccgaag 25

RESULT 11
AAH41500
ID AAH41500 standard; DNA; 32 BP.
AC AAH41500;
XX
XX DT 23-AUG-2001 (first entry)
XX
XX DE Human tyrosine kinase Hck binding protein cloning PCR primer SEQ:14.
XX
XX KW Human; tyrosine kinase Hck binding protein; tyrosine kinase; Hck;
XX KW tumour lethal factor; tumour necrosis factor alpha; apoptosis; HSB-1;
XX KW Hck signal transduction; human immunodeficiency virus; HIV infection;
XX KW anticancer; PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200132869-A1.
XX
XX PD 10-MAY-2001.
XX
XX PF 26-OCT-2000; 2000WO-JP07500.
XX
XX PR 29-OCT-1999; 95JP-0309957.
XX
XX PA (SSSE ) SSP CO LTD.
XX
XX PI Taniyama T, Narita T;
XX
XX DR WPI; 2001-316440/33.

```

```

XX
XX PT New proteins which bind to human tyrosine kinase Hck for promotion of
XX PT apoptosis and for the elucidation of the mechanism of Hck signal
XX PT transduction -
XX
XX PS Example 4; Page 41; 45pp; Japanese.
XX
XX CC The present invention describes a protein, designated HSB-1, which binds
XX CC to human tyrosine kinase Hck. Also described are: (1) nucleic acids
XX CC encoding the protein and its derivatives; (2) recombinant vectors
XX CC containing the nucleic acids; and (3) host cells transformed by the
XX CC vectors and expressing the protein. HSB-1 has cytostatic activity, binds
XX CC tyrosine kinase, enhances tumour necrosis factor alpha and promotes
XX CC apoptosis. HSB-1 proteins are used for the elucidation of the mechanism
XX CC of Hck signal transduction and of the role of Hck in human
XX CC immunodeficiency virus (HIV) infection. They can be used for the
XX CC treatment of infections and other diseases with which Hck is associated.
XX CC They promote the anticancer activity of tumour necrosis factor alpha.
XX CC The present sequence represents a PCR primer used in the cloning of
XX CC HSB-1, which is used in an example from the present invention.
XX
XX SQ Sequence 32 BP; 9 A; 4 C; 10 G; 9 T; 0 other;

Query Match 1.2%; Score 24; DB 22; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 529 gaggaagtgttttcaaggcattc 552
DB 9 gaggaagtgttttcaaggcattc 32

RESULT 12
AAC90044
ID AAC90044 standard; DNA; 78 BP.
XX
XX AC AAC90044;
XX
XX DT 13-MAR-2001 (first entry)
XX
XX DE PCR primer used to create a library of RRT-Hck SH3 domains.
XX
XX KW SH3 domain; human; Src homology region 3 domain; RT-loop; Hck protein;
XX KW PCR primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200072742-A2.
XX
XX PD 07-DEC-2000.
XX
XX PF 26-MAY-2000; 2000WO-FI00477.
XX
XX PR 26-MAY-1999; 99US-0136085.
XX
XX PA (SAKS/) SAKSELA K.
XX
XX PI Saksela K, Hilpakka M;
XX
XX DR WPI; 2001-061424/07.
XX
XX PT A method for generating Src homology region 3 (SH3) domains with
XX PT tailored binding properties or artificial SH3 domains, comprises
XX PT employing random manipulation of the SH3 RT-loop sequence -
XX
XX PS Example 1; Page 10; 34pp; English.
XX
XX CC The present invention relates to a method for generating Src homology
XX CC region 3 (SH3) domains with tailored binding properties. The method
XX CC comprises producing a collection of SH3 domains containing a randomised
XX CC RT-loop (RRT-SH3 domains). Human p59 Hck was used in the present
XX CC invention as the SH3 domain. The present sequence is a PCR primer, which

```

CC was used to create a library of RRT-Hck SH3 domains. The generated SH3
CC domains are useful for inhibiting, activating or modifying the functions
CC of cellular or pathogen-encoded proteins for research or therapeutic
CC purposes.

XX
SQ Sequence 78 BP; 13 A; 13 C; 17 G; 17 T; 18 other;

Query Match 1.2%; Score 24; DB 22; Length 78;

Best Local Similarity 100.0%; Pred. No. 0.21; Mismatches 0; Indels 0; Gaps 0;

Matches 24; Conservative 0; Indels 0; Gaps 0;
QY 391 gacctcagcttcagaaggggac 414
|||||
Db 55 gacctcagcttcagaaggggac 78

RESULT 13

AAF95624

ID AAF95624 standard; DNA; 21 BP.

XX

AC AAF95624;

XX

DT 06-JUN-2001 (first entry)

XX

DE Human gene single nucleotide polymorphism #385.

XX

KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Variation replace(11,C)

FT FT /*tag= a

FT FT /standard_name= "single nucleotide polymorphism"

XX

PN WO200118250-A2.

XX

PD 15-MAR-2001.

XX

PF 07-SEP-2000; 2000WO-US24503.

XX

PR 10-SEP-1999; 99US-0153357.

XX

PR 26-JUL-2000; 2000US-0220947.

XX

PR 16-AUG-2000; 2000US-0225724.

XX

PA (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX

PA (MILL-) MILLENNIUM PHARM INC.

XX

PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;

XX

DR WPI; 2001-226749/23.

XX

PT Nucleic acids comprising single nucleotide polymorphisms, useful in

XX applications such as forensics, paternity testing, medicine, genetic

XX analysis and phenotype correlations to diseases such as diabetes and

XX atherosclerosis -

XX Examples; Page 75; 242pp; English.

XX The present invention provides a method of diagnosing a vascular disease

XX in an individual, involving determining the sequence at various

XX polymorphic sites within the human thrombospondin 1 and thrombospondin 4

XX genes. The sequences at a number of polymorphic sites are also provided

XX in the specification. In particular, the method can be used in the

XX diagnosis of atherosclerosis, myocardial infarction, coronary heart

XX disease, stroke, peripheral vascular diseases, venous thromboembolism

XX and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also

XX useful in forensics, paternity testing, genetic analysis and phenotype

XX correlations to diseases. The present sequence is an example of one of

CC the human gene SNPs shown in the specification.

XX Sequence 21 BP; 3 A; 7 C; 6 G; 5 T; 0 other;

SQ

Query Match 1.0%; Score 21; DB 22; Length 21;

Best Local Similarity 100.0%; Pred. No. 6.3;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 ccgcgttgactctctggagac 527

|||||

Db 1 ccgcgttgactctctggagac 21

RESULT 14

AAF95625

ID AAF95625 standard; DNA; 21 BP.

XX

AC AAF95625;

XX

DT 06-JUN-2001 (first entry)

XX

DE Human gene single nucleotide polymorphism #386.

XX

KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;

KW polymorphism; vascular disease; coronary artery disease; forensics;

KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;

KW pulmonary embolism; paternity test; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Variation replace(11,T)

FT FT /*tag= a

FT FT /standard_name= "single nucleotide polymorphism"

XX

PN WO200118250-A2.

XX

PD 15-MAR-2001.

XX

PF 07-SEP-2000; 2000WO-US24503.

XX

PR 10-SEP-1999; 99US-0153357.

XX

PR 26-JUL-2000; 2000US-0220947.

XX

PR 16-AUG-2000; 2000US-0225724.

XX

PA (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX

PA (MILL-) MILLENNIUM PHARM INC.

XX

PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;

XX

DR WPI; 2001-226749/23.

XX

PT Nucleic acids comprising single nucleotide polymorphisms, useful in

XX applications such as forensics, paternity testing, medicine, genetic

XX analysis and phenotype correlations to diseases such as diabetes and

XX atherosclerosis -

XX Examples; Page 75; 242pp; English.

XX The present invention provides a method of diagnosing a vascular disease

XX in an individual, involving determining the sequence at various

XX polymorphic sites within the human thrombospondin 1 and thrombospondin 4

XX genes. The sequences at a number of polymorphic sites are also provided

XX in the specification. In particular, the method can be used in the

XX diagnosis of atherosclerosis, myocardial infarction, coronary heart

XX disease, stroke, peripheral vascular diseases, venous thromboembolism

XX and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also

XX useful in forensics, paternity testing, genetic analysis and phenotype

XX correlations to diseases. The present sequence is an example of one of

XX the human gene SNPs shown in the specification.

XX Sequence 21 BP; 8 A; 4 C; 7 G; 2 T; 0 other;

SQ

Query Match 1.0%; Score 21; DB 22; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 773 tggaccactacaagaaggga 793
 DB 1 tggaccactacaagaaggga 21

RESULT 15
 AAF95626
 ID AAF95626 standard; DNA; 21 BP.
 XX
 AC AAF95626;
 XX
 DT 06-JUN-2001 (first entry)
 XX
 DE Human gene single nucleotide polymorphism #387.
 XX
 KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
 KW polymorphism; vascular disease; coronary artery disease; forensics;
 KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
 KW pulmonary embolism; paternity test; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Variation replace(11,C)
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"
 XX
 PN WO200118250-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 07-SEP-2000; 2000WO-US24503.
 XX
 PR 10-SEP-1999; 99US-0153357.
 PR 26-JUL-2000; 2000US-0220947.
 PR 16-AUG-2000; 2000US-0225724.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JU;
 WPI; 2001-226749/23.
 XX
 PT Nucleic acids comprising single nucleotide polymorphisms, useful in
 PT applications such as forensics, paternity testing, medicine, genetic
 PT analysis and phenotype correlations to diseases such as diabetes and
 PT atherosclerosis -
 XX
 PS Examples; Page 75; 242pp; English.
 XX
 CC The present invention provides a method of diagnosing a vascular disease
 CC in an individual, involving determining the sequence at various
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
 CC genes. The sequences at a number of polymorphic sites are also provided
 CC in the specification. In particular, the method can be used in the
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism
 CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
 CC useful in forensics, paternity testing, genetic analysis and phenotype
 CC correlations to diseases. The present sequence is an example of one of
 CC the human gene SNPs shown in the specification.
 XX
 SQ Sequence 21 BP; 2 A; 5 C; 6 G; 8 T; 0 other;

Query Match 1.0%; Score 21; DB 22; Length 21;

Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 347 tcatcgtggtgcctgtatg 367
 DB 1 tcatcgtggtgcctgtatg 21

RESULT 16
 AAF95627
 ID AAF95627 standard; DNA; 21 BP.
 XX
 AC AAF95627;
 XX
 DT 06-JUN-2001 (first entry)
 XX
 DE Human gene single nucleotide polymorphism #388.
 XX
 KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
 KW polymorphism; vascular disease; coronary artery disease; forensics;
 KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
 KW pulmonary embolism; paternity test; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Variation replace(11,T)
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"
 XX
 PN WO200118250-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 07-SEP-2000; 2000WO-US24503.
 XX
 PR 10-SEP-1999; 99US-0153357.
 PR 26-JUL-2000; 2000US-0220947.
 PR 16-AUG-2000; 2000US-0225724.
 XX
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JU;
 WPI; 2001-226749/23.
 XX
 PT Nucleic acids comprising single nucleotide polymorphisms, useful in
 PT applications such as forensics, paternity testing, medicine, genetic
 PT analysis and phenotype correlations to diseases such as diabetes and
 PT atherosclerosis -
 XX
 PS Examples; Page 75; 242pp; English.
 XX
 CC The present invention provides a method of diagnosing a vascular disease
 CC in an individual, involving determining the sequence at various
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
 CC genes. The sequences at a number of polymorphic sites are also provided
 CC in the specification. In particular, the method can be used in the
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism
 CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
 CC useful in forensics, paternity testing, genetic analysis and phenotype
 CC correlations to diseases. The present sequence is an example of one of
 CC the human gene SNPs shown in the specification.
 XX
 SQ Sequence 21 BP; 7 A; 9 C; 2 G; 3 T; 0 other;

Query Match 1.0%; Score 21; DB 22; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 377 ccattaccacgaagacctca 397
 |||||
 Db 1 ccattaccacgaagacctca 21

RESULT 17

AAF95628
 ID AAF95628 standard; DNA; 21 BP.

XX AC AAF95628;

XX DT 06-JUN-2001 (first entry)

XX DE Human gene single nucleotide polymorphism #389.

XX KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
 KW polymorphism; vascular disease; coronary artery disease; forensics;
 KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
 KW pulmonary embolism; paternity test; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Variation replace(11,G)
 FT /*tag= a

FT /*standard_name= "single nucleotide polymorphism"

XX PN WO200118250-A2.

XX PD 15-MAR-2001.

XX PF 07-SEP-2000; 2000WO-US24503.

XX PR 10-SEP-1999; 99US-0153357.

XX PR 26-JUL-2000; 2000US-0220947.

XX PR 16-AUG-2000; 2000US-0225724.

XX PA (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;

XX RI WPI; 2001-226749/23.

XX DR Nucleic acids comprising single nucleotide polymorphisms, useful in
 PT applications such as forensics, paternity testing, medicine, genetic
 PT analysis and phenotype correlations to diseases such as diabetes and
 PT atherosclerosis -

XX PS Examples; Page 75; 242pp; English.

XX CC The present invention provides a method of diagnosing a vascular disease
 CC in an individual, involving determining the sequence at various
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
 CC genes. The sequences at a number of polymorphic sites are also provided
 CC in the specification. In particular, the method can be used in the
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism
 CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
 CC useful in forensics, paternity testing, genetic analysis and phenotype
 CC correlations to diseases. The present sequence is an example of one of
 CC the human gene SNPs shown in the specification.

XX SQ Sequence 21 BP; 4 A; 8 C; 8 G; 1 T; 0 other;

Query Match 1.0%; Score 21; DB 22; Length 21;

Best Local Similarity 100.0%; Pred. No. 6.3;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 461 ccctggccaccgggaaggagg 481

|||||

Db 1 ccctggccaccgggaaggagg 21

RESULT 18

AAF95629
 ID AAF95629 standard; DNA; 21 BP.

XX AC AAF95629;

XX DT 06-JUN-2001 (first entry)

XX DE Human gene single nucleotide polymorphism #390.

XX KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
 KW polymorphism; vascular disease; coronary artery disease; forensics;
 KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
 KW pulmonary embolism; paternity test; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 FT Variation replace(11,T)
 FT /*tag= a

FT /*standard_name= "single nucleotide polymorphism"

XX PN WO200118250-A2.

XX PD 15-MAR-2001.

XX PF 07-SEP-2000; 2000WO-US24503.

XX PR 10-SEP-1999; 99US-0153357.

XX PR 26-JUL-2000; 2000US-0220947.

XX PR 16-AUG-2000; 2000US-0225724.

XX PA (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;

XX RI WPI; 2001-226749/23.

XX DR Nucleic acids comprising single nucleotide polymorphisms, useful in
 PT applications such as forensics, paternity testing, medicine, genetic
 PT analysis and phenotype correlations to diseases such as diabetes and
 PT atherosclerosis -

XX PS Examples; Page 75; 242pp; English.

XX CC The present invention provides a method of diagnosing a vascular disease
 CC in an individual, involving determining the sequence at various
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
 CC genes. The sequences at a number of polymorphic sites are also provided
 CC in the specification. In particular, the method can be used in the
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism
 CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
 CC useful in forensics, paternity testing, genetic analysis and phenotype
 CC correlations to diseases. The present sequence is an example of one of
 CC the human gene SNPs shown in the specification.

XX SQ Sequence 21 BP; 4 A; 11 C; 4 G; 2 T; 0 other;

Query Match 1.0%; Score 21; DB 22; Length 21;

Best Local Similarity 100.0%; Pred. No. 6.3;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 230 ccagcgccagccacactgtc 250

|||||

Db 1 ccagcgccagccacactgtc 21

RESULT 19

AAF95630
 ID AAF95630 standard; DNA; 21 BP.
 AC AAF95630;
 XX
 XX
 DT 06-JUN-2001 (first entry)
 XX
 DE Human gene single nucleotide polymorphism #391.
 XX
 XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
 KW polymorphism; vascular disease; coronary artery disease; forensics;
 KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
 KW pulmonary embolism; paternity test; ds.
 XX
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT Variation replace(11,T)
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"
 XX
 PN WO200118250-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 07-SEP-2000; 2000WO-US24503.
 XX
 XX 10-SEP-1999; 99US-0153357.
 PR 26-JUL-2000; 2000US-0220947.
 PR 16-AUG-2000; 2000US-0225724.
 XX
 XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;
 XX WPT; 2001-226749/23.
 DR
 XX
 XX Nucleic acids comprising single nucleotide polymorphisms, useful in
 PT applications such as forensics, paternity testing, medicine, genetic
 PT analysis and phenotype correlations to diseases such as diabetes and
 PT atherosclerosis -
 XX
 XX Examples; Page 75; 242pp; English.
 PS
 XX The present invention provides a method of diagnosing a vascular disease
 CC in an individual, involving determining the sequence at various
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
 CC genes. The sequences at a number of polymorphic sites are also provided
 CC in the specification. In particular, the method can be used in the
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism
 CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
 CC useful in forensics, paternity testing, genetic analysis and phenotype
 CC correlations to diseases. The present sequence is an example of one of
 CC the human gene SNPs shown in the specification.
 XX
 SQ Sequence 21 BP; 6 A; 9 C; 3 G; 3 T; 0 other;
 XX
 Query Match 1.0%; Score 21; DB 22; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6.3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 384 ccagaagacctcagcttcca 404
 Db 1 ccagaagacctcagcttcca 21
 XX
 RESULT 20
 AAT41207
 ID AAT41207 standard; DNA; 20 BP.
 XX

AAT41207;
 AC
 XX
 DT 03-DEC-1996 (first entry)
 XX
 DE Human gene signature HUMGS01089-derived sense primer.
 XX
 XX Gene signature; messenger RNA; mRNA; relative abundance; frequency;
 KW human; cloning; mapping; non-biased library; diagnosis; detection;
 KW cell typing; abnormal cell function; primer; PCR; amplification;
 KW polymerase chain reaction; ss.
 XX
 OS Synthetic.
 XX
 XX WO9514772-A1.
 PN
 XX
 PD 01-JUN-1995.
 XX
 XX 11-NOV-1994; 94WO-JP01916.
 PF
 XX
 PR 12-NOV-1993; 93JP-0355504.
 XX
 XX (MATS/) MATSUBARA K.
 PA (OKUBO/) OKUBO K.
 XX
 XX Matsubara K, Okubo K;
 PI
 XX WPI; 1995-206931/27.
 DR
 XX Identifying gene signatures in 3'-directed human cDNA library - e.g.
 PT for diagnosis of abnormal cell function, by preparing cDNA that
 PT reflects relative abundance of corresp. mRNA in specific human
 PT tissues
 XX
 XX Example 7; Fig 8; 2245pp; Japanese.
 PS
 XX Primers T41001-T41382 are derived from novel human gene signature (GS)
 CC sequences which did not match with sequences deposited in Genbank release
 CC 76. The GS sequences (T1901-T26837) were obtained from 3'-directed cDNA
 CC libraries prepared from various human tissues; synthesis of cDNA was
 CC initiated from the 3'-end of mRNA by using poly(T) as the sole primer.
 CC Each library is constructed so as to reflect accurately the relative
 CC abundance of different mRNAs in the particular tissue from which it was
 CC derived. The appearance frequency of a given GS in a cDNA library can be
 CC determined (esp. using primers and probes derived from the GS sequences)
 CC as a means of diagnosing abnormal cell function or for recognising
 CC different cell types. The primers T41207-8 amplify clone pm0112 which
 CC comprises the GS HUMGS001089 (T20089), located on chromosome 20.
 XX
 SQ Sequence 20 BP; 4 A; 5 C; 5 G; 6 T; 0 other;
 XX
 Query Match 1.0%; Score 20; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1634 tgctggatgacttctacacg 1653
 Db 1 tgctggatgacttctacacg 20
 XX
 RESULT 21
 AAT41208/c
 ID AAT41208 standard; DNA; 20 BP.
 XX
 XX AAT41208;
 AC
 XX
 DT 03-DEC-1996 (first entry)
 XX
 DE Human gene signature HUMGS01089-derived anti-sense primer.
 XX
 XX Gene signature; messenger RNA; mRNA; relative abundance; frequency;
 KW human; cloning; mapping; non-biased library; diagnosis; detection;
 KW cell typing; abnormal cell function; primer; PCR; amplification;

KW polymerase chain reaction; ss.

XX Synthetic.

XX WO9514772-A1.

PN XX

XX PD

XX 01-JUN-1995.

XX 11-NOV-1994; 94WO-JP01916.

XX 12-NOV-1993; 93JP-0355504.

XX (MATSU) MATSUBARA K.

XX (OKUBA) OKUBO K.

XX Matsubara K, Okubo K;

XX WPI; 1995-206931/27.

XX Identifying gene signatures in 3'-directed human cDNA library - e.g.

XX for diagnosis of abnormal cell function, by preparing cDNA that

XX reflects relative abundance of corresp. mRNA in specific human

XX tissues

XX Example 7; Fig 8; 2245pp; Japanese.

XX Primers T41001-T41382 are derived from novel human gene signature (GS)

XX sequences which did not match with sequences deposited in Genbank release

XX 76. The GS sequences (T41001-T41382) were obtained from 3'-directed cDNA

XX libraries prepared from various human tissues; synthesis of cDNA was

XX initiated from the 3'-end of mRNA by using poly(T) as the sole primer.

XX Each library is constructed so as to reflect accurately the relative

XX abundance of different mRNAs in the particular tissue from which it was

XX derived. The appearance frequency of a given GS in a cDNA library can be

XX determined (esp. using primers and probes derived from the GS sequences)

XX as a means of diagnosing abnormal cell function or for recognising

XX different cell types. The primers T41207-8 amplify clone pm0112 which

XX comprises the GS HUMGS001089 (T20089), located on chromosome 20.

XX Sequence 20 BP; 2 A; 6 C; 4 G; 8 T; 0 other;

SQ

Query Match 1.0%; Score 20; DB 16; Length 20;

Best Local Similarity 100.0%; Pred. No. 19;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1673 aacagcagccatgataggga 1692

|||||

Db 20 AACAGCAGCCATGATAGGGA 1

RESULT 22

AAL33024/C

ID AAL33024 standard; DNA; 51 BP.

XX

XX AAL33024;

XX 24-JAN-2002 (first entry)

XX

XX Human SNP oligonucleotide #6232.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;

XX neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;

XX amyloid protein; angiotensin; apoptosis related protein; cadherin;

XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;

XX complement related protein; cytochrome; kinesin; cytokine; interferon;

XX interleukin; G-protein coupled receptor; thioesterase; inflammation;

XX multifactorial disease; autoimmune disease; infection;

XX nervous system disease; ss.

XX Homo sapiens.

OS

XX WO200147944-A2.

PN

XX

PD

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

05-JUL-2001.

28-DEC-2000; 2000WO-US35498.

28-DEC-1999; 99US-0173419.

27-DEC-2000; 2000US-0173419.

(CURA-) CURAGEN CORP.

Shimkets RA, Leach M;

WPI; 2001-465210/50.

Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,

oncogenes and histones, useful for diagnosing and treating, e.g.

cancer, autoimmune diseases and infections -

Claim 1; Page 3170; 4143pp; English.

The present invention relates to oligonucleotides encoding polymorphic

variants of proteins related to amylases, amyloid proteins, angiotensin,

apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,

histones, kinases, colony stimulating factors, complement related

proteins, cytochromes, kinesins, cytokines, interferons, interleukins,

G-protein coupled receptors and thioesterases. The present sequence is

one such oligonucleotide. The oligonucleotides and the peptides encoded

by them may be used in the prevention, diagnosis and treatment of

diseases associated with inappropriate expression of the proteins listed

above. Disorders that may be prevented, diagnosed and/or treated include

multifactorial diseases with a genetic component, such as autoimmune

diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, cancer

systemic lupus erythematosus and Grave's disease), inflammation, cancer

(e.g. cancers of the bladder, brain, breast, colon and kidney,

leukaemia), diseases of the nervous system and an infection of pathogenic

organisms.

Sequence 51 BP; 7 A; 14 C; 19 G; 11 T; 0 other;

Query Match 0.9%; Score 19; DB 22; Length 51;

Best Local Similarity 100.0%; Pred. No. 61;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1232 actacatccaccgagacct 1250

|||||

Db 25 ACTACATCCACCGAGACCT 7

RESULT 23

AAL33025/C

ID AAL33025 standard; DNA; 51 BP.

XX

XX AAL33025;

XX 24-JAN-2002 (first entry)

XX Human SNP oligonucleotide #6233.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;

XX neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;

XX amyloid protein; angiotensin; apoptosis related protein; cadherin;

XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;

XX complement related protein; cytochrome; kinesin; cytokine; interferon;

XX interleukin; G-protein coupled receptor; thioesterase; inflammation;

XX multifactorial disease; autoimmune disease; infection;

XX nervous system disease; ss.

XX Homo sapiens.

OS

XX WO200147944-A2.

XX

XX

XX

XX

XX PF 28-DEC-2000; 2000WO-US35498.
 XX PR 28-DEC-1999; 99US-0173419.
 XX PR 27-DEC-2000; 2000US-0173419.
 XX PA (CURA-) CURAGEN CORP.
 XX PI Shinkets RA, Leach M;
 XX DR WPI; 2001-465210/50.
 XX CC Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 XX PS Claim 1; Page 3170; 4143pp; English.
 XX CC The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinases, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.
 XX CC
 XX SQ Sequence 51 BP; 7 A; 12 C; 20 G; 12 T; 0 other;

Query Match 0.9%; Score 19; DB 22; Length 51;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1232 actacatccaccagacct 1250
 Db 24 ACTACATCCACCGAGACCT 6

RESULT 24
 AAA82879
 ID AAA82879 standard; DNA; 19 BP.
 XX AC
 XX AC AAA82879;
 XX DT 04-DEC-2000 (first entry)
 XX DE cdk4 ribozyme binding site #60.
 XX KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
 KW restenosis; ss.
 XX OS Mammalia.
 XX PN WO200032765-A2.
 XX PD 08-JUN-2000.
 XX PF 06-DEC-1999; 99WO-US28772.
 XX PR 04-DEC-1998; 98US-0110954.
 XX PA (IMMU-) IMMUSOL INC.
 XX PI Tritz R, Welch PJ, Barber JR, Robbins JM;

XX DR WPI; 2000-412314/35.
 XX PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 XX PCNA and Cyclin B1 -
 XX PS Disclosure; Page 53; 109pp; English.
 XX CC The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in
 CC AA82415 to AAA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells.
 CC The ribozyme is resistant to endonuclease activity and hence is
 CC efficient in restenosis treatment.
 XX SQ Sequence 19 BP; 1 A; 6 C; 7 G; 5 T; 0 other;

Query Match 0.9%; Score 18; DB 21; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1297 gctgactttggcctggcc 1314
 Db 2 gctgactttggcctggcc 19

RESULT 25
 AAH58041
 ID AAH58041 standard; DNA; 19 BP.
 XX AC
 XX AC AAH58041;
 XX DT 10-SEP-2001 (first entry)
 XX DE Cell-cycle dependent kinase cdk4 ribozyme binding site SEQ ID NO:465.
 XX KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnery;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX PN WO200130362-A2.
 XX PD 03-MAY-2001.
 XX PF 26-OCT-2000; 2000WO-US29500.
 XX PR 26-OCT-1999; 99US-0161532.
 XX PA (IMMU-) IMMUSOL INC.
 XX PI Robbins JM, Tritz R;
 XX DR WPI; 2001-300427/31.
 XX PT Treating proliferative skin or eye diseases and scarring, using
 PT ribozymes that cleave RNA encoding cytokines involved in inflammation,
 PT matrix metalloproteinases, growth factors and cell-cycle dependent
 PT kinases -
 XX

PS Example 1; Page 105; 408pp; English.

CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antiproliferative,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulvar, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative
CC skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention.

SQ Sequence 19 BP; 1 A; 6 C; 7 G; 5 T; 0 other;

Query Match 0.9%; Score 18; DB 22; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1297 gctgactttggcctggcc 1314

|||||

Db 2 gctgactttggcctggcc 19

RESULT 26

AAAX29342

ID AAX29342 standard; DNA; 20 BP.

AC AAX29342;

XX 10-JUN-1999 (first entry)

DE Chemically modified sense control probe ISIS No: 14318.

XX Antisense oligonucleotide; Jun N-terminal kinase; JNK; hybridise; JNK1;
KW JNK2; JNK3; cell cycle progression; phosphorylation; tumour; probe;
KW hyperproliferative disease; human; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9909214-A1.

PN 25-FEB-1999.

XX 07-AUG-1998; 98WO-US16488.

XX 13-AUG-1997; 97US-0910629.

XX (ISIS-) ISIS PHARM INC.

XX Dean N, Gaarde WA, McKay R, Monia BP, Nero PS;

PI WPI; 1999-181060/15.

DR New antisense oligonucleotides that detect and modulate the

XX expression of Jun N-terminal kinase proteins - useful for treating
PT hyperproliferative diseases and inhibiting tumor growth in animals,
PT and for modulating protein phosphorylation by these proteins
XX Example 4; Page 92; 190pp; English.

PS The invention relates to antisense oligonucleotides that detect and

XX CC

CC modulate the expression of Jun N-terminal kinase (JNK) proteins. The
CC oligonucleotides specifically hybridize to a nucleic acid encoding a
CC JNK1, JNK2 or JNK3 protein, and which modulate expression of these
CC proteins. The oligonucleotides are useful for modulating JNK protein
CC expression and cell cycle progression in cultured cells or animal cells.
CC The oligonucleotides are also useful for modulating the phosphorylation
CC of a protein that has been phosphorylated by a JNK protein, and the
CC expression of a cellular protein that promotes one or more metastatic
CC events. The oligonucleotides also form pharmaceutical compositions for
CC treating animals with a hyperproliferative disease, and for inhibiting
CC tumor growth in an animal.

XX Sequence 20 BP; 2 A; 7 C; 7 G; 4 T; 0 other;

Query Match 0.9%; Score 18; DB 20; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 gactttggcctggcccg 1317

|||||

Db 1 gactttggcctggcccg 18

RESULT 27

AAAX29331/c

ID AAX29331 standard; DNA; 20 BP.

XX AAX29331;

AC 10-JUN-1999 (first entry)

DE JNK2-specific probe ISIS No: 12560.

XX Antisense oligonucleotide; Jun N-terminal kinase; JNK; hybridise; JNK1;
KW JNK2; JNK3; cell cycle progression; phosphorylation; tumour; probe;
KW hyperproliferative disease; human; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9909214-A1.

PN 25-FEB-1999.

XX 07-AUG-1998; 98WO-US16488.

XX 13-AUG-1997; 97US-0910629.

XX (ISIS-) ISIS PHARM INC.

XX Dean N, Gaarde WA, McKay R, Monia BP, Nero PS;

PI WPI; 1999-181060/15.

DR New antisense oligonucleotides that detect and modulate the

XX expression of Jun N-terminal kinase proteins - useful for treating
PT hyperproliferative diseases and inhibiting tumor growth in animals,
PT and for modulating protein phosphorylation by these proteins
XX Example 4; Page 87; 190pp; English.

PS The invention relates to antisense oligonucleotides that detect and

XX CC
CC modulate the expression of Jun N-terminal kinase (JNK) proteins. The
CC oligonucleotides specifically hybridize to a nucleic acid encoding a
CC JNK1, JNK2 or JNK3 protein, and which modulate expression of these
CC proteins. The oligonucleotides are useful for modulating JNK protein
CC expression and cell cycle progression in cultured cells or animal cells.
CC The oligonucleotides are also useful for modulating the phosphorylation
CC of a protein that has been phosphorylated by a JNK protein, and the
CC expression of a cellular protein that promotes one or more metastatic
CC events. The oligonucleotides also form pharmaceutical compositions for
CC treating animals with a hyperproliferative disease, and for inhibiting

CC tumor growth in an animal.
 XX Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;
 SQ

Query Match 0.9%; Score 18; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 gactttggcctggcccg 1317
 |||||
 Db 20 GACTTTGGCCTGGCCCG 3

RESULT 28
 AAC62874/c
 ID AAC62874 standard; DNA; 20 BP.

XX AAC62874;
 XX AC
 XX 06-FEB-2001 (first entry)
 XX
 XX JNK antisense oligonucleotide ISIS #12560.
 DE Antisense; gene therapy; JNK2 protein; apoptosis; cancer;
 XX cellular hyperproliferation; Alzheimer's; Parkinson's disease;
 KW amyotrophic lateral sclerosis; retinitis; pigmentosa; epilepsy;
 KW myocardial infarction; stroke; obstructive jaundice; polycystic kidney;
 KW diabetes; Jun N-terminal kinase; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200059549-A1.
 PN 12-OCT-2000.
 XX
 XX 04-APR-2000; 2000WO-US08880.
 XX
 XX 07-APR-1999; 99US-0287796.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX McKay R, Dean NM, Monia BP, Nero PS, Gaarde WA;
 XX WPI; 2000-638427/61.
 XX
 XX Novel methods for reducing apoptosis comprising contacting cells with
 PT antisense oligonucleotides, useful for treating apoptotic disorders,
 PT e.g. cancer -
 XX
 XX Claim 3; Page 133; 160pp; English.

XX The present invention relates to antisense oligonucleotides
 CC (AAC62844-C63000, AAA96093-A96099 and AAA07993) that hybridise
 CC specifically to a nucleotide encoding a Jun N-terminal kinase (JNK2)
 CC protein, resulting in decrease of JNK2 expression and leading to
 CC induction of apoptosis. The present sequence is one such antisense
 CC oligonucleotide. The oligonucleotides of the present invention are useful
 CC for treating diseases or conditions with reduced apoptosis, e.g. cancer
 CC and cellular hyperproliferation. The oligonucleotides may also be used to
 CC increase the stimulation of apoptotic proteins, e.g. for treating
 CC Alzheimer's or Parkinson's disease, amyotrophic lateral sclerosis,
 CC retinitis, pigmentosa, epilepsy, myocardial infarction, stroke,
 CC obstructive jaundice, polycystic kidney and diabetes. The present
 CC sequence may have a phosphorothioate backbone.
 XX Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;
 SQ

Query Match 0.9%; Score 18; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 gactttggcctggcccg 1317
 |||||
 Db 20 GACTTTGGCCTGGCCCG 3

RESULT 29
 AAC62885
 ID AAC62885 standard; DNA; 20 BP.

XX AAC62885;
 XX AC
 XX 06-FEB-2001 (first entry)
 XX
 XX JNK antisense oligonucleotide ISIS #14318.
 DE Antisense; gene therapy; JNK2 protein; apoptosis; cancer;
 XX cellular hyperproliferation; Alzheimer's; Parkinson's disease;
 KW amyotrophic lateral sclerosis; retinitis; pigmentosa; epilepsy;
 KW myocardial infarction; stroke; obstructive jaundice; polycystic kidney;
 KW diabetes; Jun N-terminal kinase; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200059549-A1.
 PN 12-OCT-2000.
 XX
 XX 04-APR-2000; 2000WO-US08880.
 XX
 XX 07-APR-1999; 99US-0287796.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX McKay R, Dean NM, Monia BP, Nero PS, Gaarde WA;
 XX WPI; 2000-638427/61.
 XX
 XX Novel methods for reducing apoptosis comprising contacting cells with
 PT antisense oligonucleotides, useful for treating apoptotic disorders,
 PT e.g. cancer -
 XX
 XX Example 4; Page 135; 160pp; English.

XX The present invention relates to antisense oligonucleotides
 CC (AAC62844-C63000, AAA96093-A96099 and AAA07993) that hybridise
 CC specifically to a nucleotide encoding a Jun N-terminal kinase (JNK2)
 CC protein, resulting in decrease of JNK2 expression and leading to
 CC induction of apoptosis. The present sequence is one such antisense
 CC oligonucleotide. The oligonucleotides of the present invention are useful
 CC for treating diseases or conditions with reduced apoptosis, e.g. cancer
 CC and cellular hyperproliferation. The oligonucleotides may also be used to
 CC increase the stimulation of apoptotic proteins, e.g. for treating
 CC Alzheimer's or Parkinson's disease, amyotrophic lateral sclerosis,
 CC retinitis, pigmentosa, epilepsy, myocardial infarction, stroke,
 CC obstructive jaundice, polycystic kidney and diabetes. The present
 CC sequence may have a phosphorothioate backbone.
 XX Sequence 20 BP; 2 A; 7 C; 7 G; 4 T; 0 other;
 SQ

Query Match 0.9%; Score 18; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 gactttggcctggcccg 1317
 |||||
 Db 1 gactttggcctggcccg 18

RESULT 30
 AAA48651/c
 ID AAA48651 standard; DNA; 20 BP.

XX

```
AC AAA48651;
XX
XX
DT 20-SEP-2000 (first entry)
XX
DE Antisense oligonucleotide ISIS no.15354 to human JNK2 gene.
XX
XX Antisense; E-selectin; TNF alpha; cell adhesion;
KW tumour necrosis factor alpha; phosphorothioate; methoxyethoxy;
KW sepsis; rheumatoid arthritis; inflammatory; immune disease;
KW inflammatory bowel disease; allergic contact dermatitis; psoriasis;
KW diabetes; Grave's disease; allograft rejection; cancer; antibacterial;
KW immunosuppressive; antipsoriatic; antidiabetic; antithyroid;
KW cytostatic; dermatologic; antiallergic; Ha-ras; c-raf;
KW c-Jun N-terminal kinase; JNK; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH modified_base 1..6
FT /*tag= a
FT /mod_base= OTHER
FT /note= "All bases are 2'-methoxyethoxy,
FT additionally C bases are m5c"
FT modified_base 7..15
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate internucleotide linkage"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "All bases are 2'-methoxyethoxy,
FT additionally C bases are m5c"
FT
FT
XX WO200034303-A1.
XX
XX 15-JUN-2000.
XX
XX 08-DEC-1999; 99WO-US28965.
XX
XX 10-DEC-1998; 98US-0209668.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Xu XS;
XX
XX WPI; 2000-423367/36.
XX
XX Modulating cell adhesion molecule expression for treating immune or
XX inflammatory diseases involves treating cell with specific inhibitor of
XX Tumour Necrosis Factor alpha signalling molecule
XX
XX Claim 36; Page 46; 100pp; English.
XX
XX A novel method for modulating cell adhesion molecule expression
XX involves antisense inhibition of a tumour necrosis factor (TNF) alpha
XX signalling molecule. In the method TNF alpha signalling molecules
XX Ha-ras, c-raf and c-Jun N-terminal kinase (JNK)2 were inhibited by
XX antisense oligonucleotides. In addition an antisense oligonucleotide
XX to the cell adhesion molecule E-selectin was also examined. The
XX present sequence is the JNK2 antisense oligonucleotide. The
XX antisense oligonucleotides used in the method contained modifications,
XX namely phosphorothioate linkages and 2'methoxyethoxy bases. Some C
XX residues also had a 5'methyl modification. Inhibitors of the TNF alpha
XX signalling molecules have antibacterial, immunosuppressive,
XX antipsoriatic, antidiabetic, antithyroid, cytostatic, dermatological,
XX antiallergic and antiinflammatory activity. The antisense inhibitors
XX may be useful for the treatment of sepsis, rheumatoid arthritis,
XX inflammatory, immune disease, inflammatory bowel disease, allergic
XX contact dermatitis, psoriasis, diabetes, Grave's disease, allograft
XX rejection and cancer.
XX
XX Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;

Query Match 0.9%; Score 18; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 gactttggcctggccgg 1317
DB 20 GACTTTGGCCTGGCCCGG 3
|||||
RESULT 31
AAH23754/c
ID AAH23754 standard; DNA: 20 BP.
XX
XX AAH23754;
XX
XX 13-AUG-2001 (first entry)
XX
XX JNK1 antisense oligonucleotide, JNK2AS, (ISIS #12560).
XX
XX JNK; jun kinase; antisense; cytostatic; cancer;
KW 2'-O-methoxyethyl oligonucleotide; MOE; phosphorothioate; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= "OTHER"
FT /note= "This oligonucleotide is a 2'-O-methoxyethyl (MOE)
FT chimeric antisense oligonucleotide containing five
FT MOE/phosphodiester residues flanking a
FT 2'-deoxynucleotide/phosphorothioate region"
FT
XX WO200134792/A2.
XX
XX 17-MAY-2001.
XX
XX 10-NOV-2000; 2000WO-US30869.
XX
XX 12-NOV-1999; 99US-0165224.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Potapova O, Gorospe M, Holbrook NJ;
XX
XX WPI; 2001-335925/35.
XX
XX Use of Jun Kinase antisense mRNA for treating cancer by administering
XX vector comprising promoter operably linked to DNA sequence that encodes
XX the antisense mRNA to patient diagnosed with cancer
XX
XX Claim 1; Page 41; 75pp; English.
XX
XX The present invention relates to the use of Jun Kinase (JNK) antisense
XX oligonucleotides for treating cancer and for screening compounds that
XX mimic or augment the effect of JNK antisense oligonucleotides treatment
XX for cancer. The present sequence is one such JNK antisense
XX oligonucleotide.
XX
XX Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;

Query Match 0.9%; Score 18; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 gactttggcctggccgg 1317
DB 20 GACTTTGGCCTGGCCCGG 3
|||||
RESULT 32
```

AAF99183/c
 ID AAF99183 standard; DNA; 20 BP.
 AC AAF99183;
 XX
 DT 12-JUN-2001 (first entry)
 XX
 DE Immunostimulatory nucleic acid #299.
 XX
 KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
 KW immunostimulatory; tumour; viral infection; bacterial infection;
 KW fungal infection; parasitic infection; cancer; asthma;
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
 XX
 OS Synthetic.
 XX
 PN WO200122972-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 25-SEP-2000; 2000WO-US26383.
 XX
 PR 25-SEP-1999; 99US-0156113.
 PR 27-SEP-1999; 99US-0156135.
 PR 23-AUG-2000; 2000US-0227436.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 PA (COLE-) COLEY PHARM GMBH.
 XX
 PI Krieg AM, Schetter C, Vollmer J;
 XX
 DR WPI; 2001-273485/28.
 XX
 PT Vaccinating against tumors, infectious diseases, allergies and asthma
 PT using immunostimulatory Py-rich and TG nucleic acids .
 XX
 PS Claim 101; Page 44; 338pp; English.
 XX
 CC The present invention relates to a method for stimulating an immune
 CC response. The method comprises administering an immunostimulatory nucleic
 CC acid to a non-rodent subject in sufficient quantity to stimulate an
 CC immune response. The present sequence is one such immunostimulatory
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
 CC also useful for preventing cancer, asthma, infectious disease, allergy or
 CC immune deficiency. The present sequence can also be used to redirect a
 CC Th2 to a Th1 immune response and to activate immune cells.
 CC Note: the present sequence may have a phosphorothioate backbone.
 XX
 SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;

Query Match 0.9%; Score 18; DB 22; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 gactttggcctggcccg 1317
 |||||||||
 DB 20 GACTTTGGCCTGGCCCG 3

RESULT 33
 AAH41497
 ID AAH41497 standard; DNA; 34 BP.
 XX
 AC AAH41497;
 XX
 DT 23-AUG-2001 (first entry)
 XX

Human tyrosine kinase Hck PCR primer SEQ ID NO:9.
 DE
 XX Human; tyrosine kinase Hck binding protein; tyrosine kinase; Hck;
 KW tumour lethal factor; tumour necrosis factor alpha; apoptosis; HSB-1;
 KW Hck signal transduction; human immunodeficiency virus; HIV infection;
 KW anticancer; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200132869-A1.
 XX
 PD 10-MAY-2001.
 XX
 PF 26-OCT-2000; 2000WO-JP07500.
 XX
 PR 29-OCT-1999; 99JP-0309957.
 XX
 PA (SSSE) SSP CO LTD.
 XX
 PI Taniyama T, Narita T;
 XX
 DR WPI; 2001-316440/33.
 XX
 PT New proteins which bind to human tyrosine kinase Hck for promotion of
 PT apoptosis and for the elucidation of the mechanism of Hck signal
 PT transduction .
 XX
 PS Example 3; Page 33; 45pp; Japanese.
 XX
 CC The present invention describes a protein, designated HSB-1, which binds
 CC to human tyrosine kinase Hck. Also described are: (1) nucleic acids
 CC encoding the protein and its derivatives; (2) recombinant vectors
 CC containing the nucleic acids; and (3) host cells transformed by the
 CC vectors and expressing the protein. HSB-1 has cytostatic activity, binds
 CC tyrosine kinase, enhances tumour necrosis factor alpha and promotes
 CC apoptosis. HSB-1 proteins are used for the elucidation of the mechanism
 CC of Hck signal transduction and of the role of Hck in human
 CC immunodeficiency virus (HIV) infection. They can be used for the
 CC treatment of infections and other diseases with which Hck is associated.
 CC They promote the anticancer activity of tumour necrosis factor alpha.
 CC The present sequence represents a PCR primer for the human tyrosine
 CC kinase Hck, which is used in an example from the present invention.
 XX
 SQ Sequence 34 BP; 8 A; 8 C; 9 G; 9 T; 0 other;

Query Match 0.9%; Score 18; DB 22; Length 34;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 atgaagtcccaagttcttc 195
 |||||||||
 DB 17 atgaagtcccaagttcttc 34

RESULT 34
 AAA82878
 ID AAA82878 standard; DNA; 19 BP.
 XX
 AC AAA82878;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE cdk4 ribozyme binding site #59.
 XX
 KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic;
 KW restenosis; ss.
 XX
 OS Mammalia.
 XX
 PN WO200032765-A2.
 XX
 PD 08-JUN-2000.

XX PF 06-DEC-1999; 99WO-US28772.
 XX PR 04-DEC-1998; 98US-0110954.
 XX PA (IMMU-) IMMUSOL INC.
 XX PI Tritz R, Welch PJ, Barber JR, Robbins JM;
 XX WPI; 2000-412314/35.
 XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PT PCNA and Cyclin B1
 XX Disclosure; Page 53; 109pp; English.
 XX The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in
 CC AA82415 to AA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells.
 CC The ribozyme is resistant to endonuclease activity and hence is
 CC efficient in restenosis treatment.
 XX Sequence 19 BP; 1 A; 5 C; 7 G; 6 T; 0 other;
 SQ

Query Match 0.8%; Score 17; DB 21; Length 19;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1297 gctgactttggcctggc 1313
 Db 3 gctgactttggcctggc 19
 |||||

RESULT 35
 AAH58040
 ID AAH58040 standard; DNA; 19 BP.
 XX
 AC AAH58040;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Cell-cycle dependent kinase cdk4 ribozyme binding site SEQ ID NO:464.
 XX Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnery;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antiproliferative; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antitumor; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200130362-A2.
 XX
 PD 03-MAY-2001.
 XX
 XX 26-OCT-2000; 2000WO-US29500.
 XX
 PR 26-OCT-1999; 99US-0161532.
 XX
 PA (IMMU-) IMMUSOL INC.
 XX
 PI Robbins JM, Tritz R;

XX WPI; 2001-300427/31.
 XX Treating proliferative skin or eye diseases and scarring, us;
 PT ribozymes that cleave RNA encoding cytokines involved in infl
 PT matrix metalloproteinases, growth factors and cell-cycle depen
 PT kinases -
 XX
 XX Example 1; Page 105; 408pp; English.
 XX
 XX The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antiproliferative,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
 CC ophthalmological, vulnery, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative
 CC skin diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH57577 to AAH62099 represent sequences used in the
 CC exemplification of the present invention.
 XX
 XX Sequence 19 BP; 1 A; 5 C; 7 G; 6 T; 0 other;
 SQ

Query Match 0.8%; Score 17; DB 22; Length 19;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1297 gctgactttggcctggc 1313
 Db 3 gctgactttggcctggc 19
 |||||

Search completed: May 17, 2002, 18:25:28
 Job time: 6922 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 17, 2002, 16:26:59 ; Search time 90.41 Seconds
(without alignments)
5474.522 Million cell updates/sec

Title: US-10-007-010-3
Perfect score: 2015
Sequence: 1 cggaggcgcgaagatgag.....ataataatgcaagtcttacg 2015

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 0

Total number of hits satisfying chosen parameters: 615614

Minimum DB seq length: 0
Maximum DB seq length: 105

Post-processing: Listing first 65 summaries

Database : Issued_Patents_NA: *
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	0.9	20	US-08-910-629A-31	Sequence 31, Appl
2	18	0.9	20	US-08-910-629A-42	Sequence 42, Appl
3	18	0.9	20	US-09-209-568-7	Sequence 7, Appl
4	18	0.9	20	US-09-287-796-31	Sequence 31, Appl
5	18	0.9	20	US-09-287-796-42	Sequence 42, Appl
6	18	0.9	20	US-09-130-616-31	Sequence 31, Appl
7	18	0.9	20	US-09-130-616-42	Sequence 42, Appl
8	17	0.8	20	US-08-730-876-2	Sequence 2, Appl
9	17	0.8	20	US-09-490-692-71	Sequence 71, Appl
10	17	0.8	23	US-08-222-616-2	Sequence 2, Appl
11	17	0.8	23	PCT-US95-04228-2	Sequence 2, Appl
12	16	0.8	24	US-08-859-998-598	Sequence 598, App
13	16	0.8	24	US-09-225-928-598	Sequence 598, App
14	15	0.7	18	US-08-951-923-51	Sequence 51, Appl
15	15	0.7	18	US-08-584-040-6218	Sequence 6218, Ap
16	15	0.7	19	US-08-400-580A-11	Sequence 11, Appl
17	15	0.7	31	US-08-942-423-51	Sequence 51, Appl
18	15	0.7	36	US-08-951-923-52	Sequence 52, Appl
19	15	0.7	36	US-08-724-586-3	Sequence 3, Appl
20	15	0.7	36	US-09-421-632-3	Sequence 3, Appl
21	15	0.7	45	US-08-039-198B-3	Sequence 3, Appl
22	15	0.7	72	US-08-707-237A-47	Sequence 47, Appl
23	15	0.7	104	US-09-058-389A-19	Sequence 19, Appl
24	15	0.7	105	US-09-461-697-78	Sequence 78, Appl
25	14	0.7	17	US-08-584-040-7661	Sequence 7661, Ap
26	14	0.7	18	US-08-105-483-197	Sequence 197, App
27	14	0.7	18	US-08-220-151-78	Sequence 78, Appl

c 28	14	0.7	18	1	US-08-413-118-78	Sequence 78, Appl
c 29	14	0.7	18	1	US-08-224-657-54	Sequence 54, Appl
c 30	14	0.7	18	1	US-08-709-209-197	Sequence 197, App
c 31	14	0.7	18	1	US-08-458-101-197	Sequence 197, App
c 32	14	0.7	18	2	US-08-184-009-52	Sequence 52, Appl
c 33	14	0.7	18	2	US-08-173-489C-11	Sequence 11, Appl
c 34	14	0.7	18	2	US-08-417-210A-52	Sequence 52, Appl
c 35	14	0.7	18	2	US-08-585-684B-2737	Sequence 2737, Ap
c 36	14	0.7	18	2	US-08-458-356-52	Sequence 52, Appl
c 37	14	0.7	18	3	US-08-473-445-78	Sequence 78, Appl
c 38	14	0.7	18	4	US-09-038-073-2737	Sequence 2737, Ap
c 39	14	0.7	18	4	US-08-460-736-52	Sequence 52, Appl
c 40	14	0.7	18	4	US-09-354-138-54	Sequence 54, Appl
c 41	14	0.7	20	1	US-08-639-763-6	Sequence 6, Appl
c 42	14	0.7	21	1	US-08-056-200-44	Sequence 44, Appl
c 43	14	0.7	21	2	US-08-800-644-44	Sequence 44, Appl
c 44	14	0.7	21	3	US-08-953-094-66	Sequence 66, Appl
c 45	14	0.7	22	1	US-07-955-916-2	Sequence 2, Appl
c 46	14	0.7	22	1	US-08-379-078-549	Sequence 549, App
c 47	14	0.7	22	4	PCT-US93-00977-172	Sequence 172, App
c 48	14	0.7	22	5	US-07-842-349-17	Sequence 17, Appl
c 49	14	0.7	24	1	US-08-151-574-39	Sequence 39, Appl
c 50	14	0.7	24	1	US-08-391-000-39	Sequence 39, Appl
c 51	14	0.7	24	2	US-08-480-994-15	Sequence 15, Appl
c 52	14	0.7	24	2	US-08-616-844-15	Sequence 15, Appl
c 53	14	0.7	24	2	US-08-419-448-39	Sequence 39, Appl
c 54	14	0.7	24	2	US-07-952-853-8	Sequence 8, Appl
c 55	14	0.7	24	2	US-08-741-931-39	Sequence 39, Appl
c 56	14	0.7	24	2	US-08-599-654-15	Sequence 15, Appl
c 57	14	0.7	24	2	US-08-485-573-15	Sequence 15, Appl
c 58	14	0.7	24	2	US-08-914-848-8	Sequence 8, Appl
c 59	14	0.7	24	3	US-08-944-868A-15	Sequence 15, Appl
c 60	14	0.7	24	3	US-08-944-423A-15	Sequence 15, Appl
c 61	14	0.7	24	3	US-08-925-743-15	Sequence 15, Appl
c 62	14	0.7	24	3	US-08-944-496-15	Sequence 15, Appl
c 63	14	0.7	24	4	US-08-925-767-15	Sequence 15, Appl
c 64	14	0.7	24	4	US-09-233-510-39	Sequence 39, Appl
c 65	14	0.7	24	4		

ALIGNMENTS

RESULT 1
US-08-910-629A-31/c
; Sequence 31, Application US/08910629A
; Patent No. 5877309 .
; GENERAL INFORMATION:
; APPLICANT: Robert A. McKay
; APPLICANT: Nicholas M. Dean
; APPLICANT: Brett Monia
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF JNK
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
; MEDIUM TYPE: STORAGE
; COMPUTER: PENTIUM
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910, 629A
; FILING DATE: August 13, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

```
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0215
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; US-08-910-629A-31

Query Match 0.9%; Score 18; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 gactttggcctggcccg 1317
| | | | | | | | | | | | | | | | | |
Db 20 GACTTTGGCTGGCCCG 31

RESULT 2
US-08-910-629A-42
; Sequence 42, Application US/08910629A
; Patent No. 5877309
; GENERAL INFORMATION:
; APPLICANT: Robert A. McKay
; APPLICANT: Nicholas M. Dean
; APPLICANT: Brett Monia
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF JNK
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
; MEDIUM TYPE: STORAGE
; COMPUTER: PENTUM
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,629A
; FILING DATE: August 13, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0215
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear

; APPLICATION NUMBER: No
; US-08-910-629A-42

Query Match 0.9%; Score 18; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 gactttggcctggcccg 1317
| | | | | | | | | | | | | | | | | |
Db 1 GACTTTGGCTGGCCCG 18

RESULT 3
US-09-209-668-7/c
; Sequence 7, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
; TITLE OF INVENTION: ALPHA-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
; FILE REFERENCE: ISPH-0336
; CURRENT APPLICATION NUMBER: US/09/209,668A
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
; US-09-209-668-7

Query Match 0.9%; Score 18; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 gactttggcctggcccg 1317
| | | | | | | | | | | | | | | | | |
Db 20 GACTTTGGCTGGCCCG 3

RESULT 4
US-09-287-796-31/c
; Sequence 31, Application US/09287796A
; Patent No. 6133246
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
; FILE REFERENCE: ISPH-0350
; CURRENT APPLICATION NUMBER: US/09/287,796A
; CURRENT FILING DATE: 1999-04-07
; EARLIER APPLICATION NUMBER: 09/130,616
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
; US-09-287-796-31
```

Query Match 0.9%; Score 18; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 gactttggcctggcccg 1317
| | | | | | | | | | | | | | | | | | | | | |
DB 20 GACTTTGGCCTGGCCCGG 3

RESULT 5
US-09-287-796-42
; Sequence 42, Application US/09287796A
; Patent No. 6133246
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; FILE REFERENCE: ISPH-0350
; CURRENT APPLICATION NUMBER: US/09/287,796A
; CURRENT FILING DATE: 1999-04-07
; EARLIER APPLICATION NUMBER: 09/130,616
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-287-796-42

Query Match 0.9%; Score 18; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 gactttggcctggcccg 1317
| | | | | | | | | | | | | | | | | | | | | |
DB 1 gactttggcctggcccg 18

RESULT 6
US-09-130-616-31/c
; Sequence 31, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; FILE REFERENCE: ISPH-0318
; CURRENT APPLICATION NUMBER: US/09/130,616C
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-130-616-31

Query Match 0.9%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 gactttggcctggcccg 1317
| | | | | | | | | | | | | | | | | | | | | |
DB 20 GACTTTGGCCTGGCCCGG 3

RESULT 7
US-09-130-616-42
; Sequence 42, Application US/09130616C
; Patent No. 6221850
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; FILE REFERENCE: ISPH-0318
; CURRENT APPLICATION NUMBER: US/09/130,616C
; CURRENT FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-130-616-42

Query Match 0.9%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 gactttggcctggcccg 1317
| | | | | | | | | | | | | | | | | | | | | |
DB 1 gactttggcctggcccg 18

RESULT 8
US-08-730-876-2/c
; Sequence 2, Application US/08730876
; Patent No. 5859314
; GENERAL INFORMATION:
; APPLICANT: HIBBS, Margaret L.;
; APPLICANT: DUNN, Ashley R.;
; APPLICANT: GRAILL, Dianne;
; APPLICANT: HODGSON George;
; APPLICANT: TARLINGTON, David M.;
; APPLICANT: ARMES, Jane
; TITLE OF INVENTION: ANIMALS WITH TARGETED GENE DELETION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44mb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/730,876
FILING DATE: 18-Oct-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,578
FILING DATE: 20-Oct-1995
ATTORNEY/AGENT INFORMATION:
NAME: No. 5859314man D. Hanson
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5369 - JEL/NDH/SLR
TELEPHONE: (212) 688-9200
TELEFAX: (212) 688-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-730-876-2

Query Match 0.8%; Score 17; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 916 gggcagtttgggaagt 932
Db 17 GGGCAGTTTGGGAAGT 1

RESULT 9
US-09-490-692-71/c
Sequence 71, Application US/09490692
Patent No. 6180353
GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
APPLICANT: Lex M. Cowsett
TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
FILE REFERENCE: RTS-0120
CURRENT APPLICATION NUMBER: US/09/490,692
CURRENT FILING DATE: 2000-01-24
NUMBER OF SEQ ID NOS: 176
SEQ ID NO 71
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-490-692-71

Query Match 0.8%; Score 17; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 tcaggaggatgatgaag 44
Db 18 TCAGGAGGATGATGAAG 2

RESULT 10
US-08-222-616-2/c
Sequence 2, Application US/08222616
Patent No. 5635177
GENERAL INFORMATION:
APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST

TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,616
FILING DATE: 4-APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00586
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/826935
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 821P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-222-616-2

Query Match 0.8%; Score 17; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1420 gacgtctggtccttgg 1436
Db 23 GAGGTCTGCTCTTGG 7

RESULT 11
PCT-US95-04228-2/c
Sequence 2, Application PC/TUS9504228
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: patin (Genentech)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/04228
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/222616
;; FILING DATE: 04-APR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wendy M. Lee
;; REGISTRATION NUMBER: 00,000
;; REFERENCE/DOCKET NUMBER: 821P3PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415/225-1994
;; TELEFAX: 415/952-9881
;; TELEX: 910/371-7168
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 23 bases
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; PCT-US95-04228-2

Query Match 0.8%; Score 17; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1420 gacgtctggtccttgg 1436
|||||

Db 23 GACGCTGCTCCTTGG 7

RESULT 12

US-08-859-998-598
; Sequence 598, Application US/0885998
; Patent No. 5994076
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,998
; FILING DATE: 21-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 598:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 24 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
;; FEATURE:
;; OTHER INFORMATION: oligonucleotide primer
;; US-08-859-998-598

Query Match 0.8%; Score 16; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1236 catccaccgagacctc 1251
|||||

Db 8 CATCCACCGAGACCTC 23

RESULT 13

US-09-225-928-598
; Sequence 598, Application US/09225928
; Patent No. 6352829
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Jokhadze, George
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1375
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: US
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,928
; FILING DATE: 05-Jan-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/859,998
; FILING DATE: 21-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Field, Bret E.
; REGISTRATION NUMBER: 37,620
; REFERENCE/DOCKET NUMBER: 09096/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-322-5070
; TELEFAX: 415-854-0875
; INFORMATION FOR SEQ ID NO: 598:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; SEQUENCE DESCRIPTION: SEQ ID NO: 598:
; US-09-225-928-598

Query Match 0.8%; Score 16; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1236 catccaccgagacctc 1251
|||||
Db 8 CATCCACGAGACCTC 23

RESULT 14

US-08-951-923-51/c
; Sequence 51, Application US/08951923
; Patent No. 6048693
; GENERAL INFORMATION:
; APPLICANT: Bitter, Grant
; TITLE OF INVENTION: PHENOTYPIC ASSAYS OF CYCLIN/CYCLIN-DEPENDENT KINASE
; TITLE OF INVENTION: FUNCTION
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward LLP
; STREET: 5 Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,923
; FILING DATE: October 16, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard L.
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: BITT-001/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650 843-5000
; TELEFAX: 650 857-0863
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18
; TYPE: nucleic acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-951-923-51

Query Match 0.7%; Score 15; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1300 gactttggcctggcc 1314
|||||
Db 18 GACTTTGGCCTGGCC 4

RESULT 15

US-08-584-040-6218/c
; Sequence 6218, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL

; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 6218:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-6218

Query Match 0.7%; Score 15; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 666 cgacctcgccagg 680
|||||
Db 18 CGACCTCGGCAGG 4

RESULT 16

US-08-400-580A-11
; Sequence 11, Application US/08400580A
; Patent No. 5693501
; GENERAL INFORMATION:
; APPLICANT: Lee, Chao-Hung
; APPLICANT: Jiang, Bingdong
; TITLE OF INVENTION: Compounds and Methods To Determine
; TITLE OF INVENTION: Presence of Histoplasma Capsulatum
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kristine H. Johnson
; STREET: 123 No. 5693501th College Ave, Ste 213
; CITY: Fort Collins
; STATE: CO
; COUNTRY: USA
; ZIP: 80524
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/400,580A


```

1  ZIP: 94303
2  COMPUTER READABLE FORM:
3  MEDIUM TYPE: Floppy disk
4  COMPUTER: IBM PC compatible
5  OPERATING SYSTEM: PC-DOS/MS-DOS
6  SOFTWARE: PatentIn Release #1.0,
7  CURRENT APPLICATION DATA:
8  APPLICATION NUMBER: US/08/942,423
9  FILING DATE: 01-OCT-1997
10 CLASSIFICATION: 435
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: US 08/362,715
13 FILING DATE: 23-DEC-1994
14 ATTORNEY/AGENT INFORMATION:
15 NAME: Perles, Rohan
16 REGISTRATION NUMBER: 35,752
17 REFERENCE/DOCKET NUMBER: 28260
18 TELECOMMUNICATION INFORMATION:
19 TELEPHONE: (415) 852-1698
20 TELEFAX: (415) 496-3529
21 INFORMATION FOR SEQ ID NO: 51:
22 SEQUENCE CHARACTERISTICS:
23 LENGTH: 31 base pairs
24 TYPE: nucleic acid
25 STRANDEDNESS: single
26 TOPOLOGY: linear
27 MOLECULE TYPE: other nucleic acid
28 DESCRIPTION: /desc = "PCR primer"
29 US-08-942-423-51

```

RESULT 19
US-08-724-586-3/c
Sequence 3, Application US/08724586
Patent No. 6086469
GENERAL INFORMATION:
APPLICANT: Kruzecki, Marian L.
APPLICANT: Kruzecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Doyle, Darrell J.

;; TITLE OF INVENTION: Cloning, Expression, and Uses of Human
;; TITLE OF INVENTION: Lactoferrin
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Jacobson, Price, Holman & Stern
;; STREET: 400 Seventh St. N.W.
;; CITY: Washington D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/724,586
;; FILING DATE: 30-SEPT-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/238,445
;; FILING DATE: 05-MAY-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Player, William E.
;; REGISTRATION NUMBER: 31,409
;; REFERENCE/DOCKET NUMBER: 10505/P58185C
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 638-6666
;; TELEFAX: (202) 393-5350
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 36 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; US-08-724-586-3

Query Match 0.7%; Score 15; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1460 cctacgcccggatcc 1474
|||||
Db 18 CCTACGCCGGATCC 4

RESULT 20
US-09-421-632-3/c
; Sequence 3, Application US/09421632
; Patent No. 6277817
; GENERAL INFORMATION:
; APPLICANT: Kruzel, Marian L.
; APPLICANT: Kurecki, Tomasz
; APPLICANT: Gollnick, Paul D.
; APPLICANT: Doyle, Darrell J.
; TITLE OF INVENTION: Cloning, Expression, and Uses of Human
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/421,632
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/724,586
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Player, William E.
;; REGISTRATION NUMBER: 31,409
;; REFERENCE/DOCKET NUMBER: 10505/P58185C
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 638-6666
;; TELEFAX: (202) 393-5350
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 36 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; US-09-421-632-3

Query Match 0.7%; Score 15; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1460 cctacgcccggatcc 1474
|||||
Db 18 CCTACGCCGGATCC 4

RESULT 21
US-08-039-198B-3/c
; Sequence 3, Application US/08039198B
; Patent No. 5858725
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PREPARATION OF CHIMAERIC ANTIBODIES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHIVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/039,198B
; FILING DATE: 29-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01744
; FILING DATE: 08-OCT-91
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1430-86
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: ssDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-039-198B-3

Query Match 0.7%; Score 15; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 745 agacacttcagcact 759
DB 33 AGCACCTTCAGCACT 19
|||||

RESULT 22
US-08-707-237A-47
; Sequence 47, Application US/08707237A
; Patent No. 5830713
; GENERAL INFORMATION:
; APPLICANT: Ferrari, Franco A.
; APPLICANT: Capello, Joseph
; APPLICANT: Crissman, John W.
; APPLICANT: Dorman, Mary A.
; TITLE OF INVENTION: METHODS FOR PREPARING SYNTHETIC
; TITLE OF INVENTION: REPETITIVE DNA
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/707,237A
; FILING DATE: 03-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,155
; FILING DATE: 29-DEC-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/053,049
; FILING DATE: 22-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/609,716
; FILING DATE: 06-NOV-1990
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/269,429
; FILING DATE: 09-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/114,618
; FILING DATE: 29-OCT-1987
; APPLICATION DATA:
; APPLICATION NUMBER: US 06/927,258
; FILING DATE: 04-NOV-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-55186-10/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 47:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 72 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-707-237A-47

Query Match 0.7%; Score 15; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1748 catccgccagggccc 1762
DB 27 CATCGCCAGGGCCC 41
|||||

RESULT 23
US-09-058-389A-19
; Sequence 19, Application US/09058389A
; Patent No. 6130065
; GENERAL INFORMATION:
; APPLICANT: Belt, Judith A.
; APPLICANT: Crawford, Charles R.
; APPLICANT: Patel, Divyen
; TITLE OF INVENTION: A NITROBENZYL MERCAPTOPURINERIBOSIDE
; TITLE OF INVENTION: (NBMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
; TITLE OF INVENTION: PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
; TITLE OF INVENTION: USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/058,389A
; FILING DATE: April 9, 1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-013N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "intron 9"
; HYPOTHETICAL: NO
US-09-058-389A-19

Query Match 0.7%; Score 15; DB 3; Length 104;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1700 ggcagggcaggggggt 1714
|||||

Db 24 GGCAGGCGAGGGGT 38

RESULT 24

US-09-461-697-78/C
; Sequence 78, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Purnam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461.697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 105
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-78

Query Match 0.7%; Score 15; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 atggctcagggga 89

|||||

Db 75 ATGGCTCTGAGGGA 61

RESULT 25

US-08-584-040-7661
; Sequence 7661, Application US/08584040
; Patent No. 6346398
; GENERAL INFORMATION:
; APPLICANT: Pavco, Pamela
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES OR
; TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
; TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 8502
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584.040
; FILING DATE: January 11, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/005,974
; FILING DATE: October 26, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/064
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7661:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-584-040-7661

Query Match 0.7%; Score 14; DB 4; Length 17;
Best Local Similarity 71.4%; Pred. No. 2.2e+03;
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1300 gactttggcctggc 1313

|||||

Db 4 GACUUGGCCUGGC 17

RESULT 26

US-08-105-483-197/C
; Sequence 197, Application US/08105483
; Patent No. 5494807
; GENERAL INFORMATION:
; APPLICANT: Paolletti, Enzo
; TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
; TITLE OF INVENTION: STRAIN
; NUMBER OF SEQUENCES: 462
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; ADDRESSEE: c/o William S. Frommer
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/105,483
; FILING DATE: 12-AUG-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,951
; FILING DATE: 06-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2400
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 197:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-105-483-197

Query Match 0.7%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 gatgaagacgatga 69
|||||
Db 14 GATGAAGACGATGA 1

RESULT 27

US-08-220-151-78/c
; Sequence 78, Application US/08220151
; Patent No. 5529780
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Limbach, Keith J.
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
; TITLE OF INVENTION: CANINE HERPESVIRUS gB, gC AND gD AND USES THEREFOR
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/220,151
; FILING DATE: 30-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2540
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; TELEX: 425066 CURTMS
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-220-151-78

Query Match 0.7%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 gatgaagacgatga 69
|||||
Db 14 GATGAAGACGATGA 1

RESULT 28

US-08-413-118-78/c
; Sequence 78, Application US/08413118
; Patent No. 5688920
; GENERAL INFORMATION:
; APPLICANT: PAOLETTI, ENZO
; APPLICANT: LIMBACH, KEITH J.
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF
; TITLE OF INVENTION: CANINE HERPESVIRUS gB, gC, AND gD AND USES THEREFOR
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
; STREET: 530 FIFTH AVENUE, 25TH FLOOR
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/413,118
; FILING DATE: 29-MAR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/220,151
; FILING DATE: 30-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FROMMER, WILLIAM S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2670
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-413-118-78

Query Match 0.7%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 gatgaagacgatga 69
|||||
Db 14 GATGAAGACGATGA 1

RESULT 29

US-08-224-657-54/c
; Sequence 54, Application US/08224657
; Patent No. 5756102
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Taylor, Jill
; TITLE OF INVENTION: POXVIRUS - CANINE DISTEMPER VIRUS (CDV)
; TITLE OF INVENTION: RECOMBINANTS AND COMPOSITIONS AND METHODS EMPLOYING THE
; TITLE OF INVENTION: RECOMBINANTS
; NUMBER OF SEQUENCES: 122
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/224,657
; FILING DATE: 06-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2550
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066 CORTMS
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-224-657-54

Query Match 0.7%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 gatgaagacgatga 69
| | | | | | | | | | | | | | | | | |
Db 14 GATGAGACGATGA 1

RESULT 30
US-08-709-209-197/c
Sequence 197, Application US/08709209
Patent No. 5762938
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 462
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,209
FILING DATE: 21-AUG-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/105,483
FILING DATE: 12-AUG-1993
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 197:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-709-209-197

Query Match 0.7%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 gatgaagacgatga 69
| | | | | | | | | | | | | | | | | |
Db 14 GATGAGACGATGA 1

RESULT 31
US-08-458-101-197/c
Sequence 197, Application US/08458101
Patent No. 5766599
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
APPLICANT: Perkus, Marion E.
APPLICANT: Taylor, Jill
APPLICANT: Tartaglia, James
APPLICANT: No. 5766599ton, Elizabeth K.
APPLICANT: Riviere, Michel
APPLICANT: de Taisne, Charles
APPLICANT: Limbach, Keith J.
APPLICANT: Johnson, Gerard P.
APPLICANT: Pincus, Steven E.
APPLICANT: Cox, William I.
APPLICANT: Audonnet, Jean-Christophe Francis
APPLICANT: Gettig, Russell Robert
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,101
FILING DATE: 01-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2740
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 197:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-458-101-197

Query Match 0.7%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 gatgaagacgatga 69
| | | | | | | | | | | | | | | | | |
Db 14 GATGAGACGATGA 1

RESULT 32

US-08-184-009-52/c
; Sequence 52, Application US/08184009
; Patent No. 5833975
; GENERAL INFORMATION:
; APPLICANT: Paolletti, Enzo
; APPLICANT: Tartaglia, James
; APPLICANT: Cox, William I.
; TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY
; NUMBER OF SEQUENCES: 217
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/184,009
; FILING DATE: 19-JAN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2530
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; TELEX: 425066CURTMS
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-184-009-52

Query Match 0.7%; Score 14; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 gatgaagacgatga 69
|||||
Db 14 GATGAAGACGATGA 1

RESULT 33
US-08-173-489C-11
; Sequence 11, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2

SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
DESCRIPTION: c-myc gene (Accession # X00364,
DESCRIPTION: K01908, V00501) nucleotides 6663 to 6680
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Gazin, C, Dupont, S, de Dinechin, D,
AUTHORS: Hampe, A, Masson, J M, Martin, P, Stehelin,
AUTHORS: D, Galibert, F.
TITLE: Nucleotide sequence of the
TITLE: human c-myc locus: provocative open reading
TITLE: frame within the first exon.
JOURNAL: EMBO Journal
VOLUME: 3
PAGES: 383-387
DATE: 1984
AUTHORS: Colby, W W, Chen, E Y, Smith, D H,
AUTHORS: Levinson, A D.
TITLE: Identification and nucleotide
TITLE: sequence of a human locus homologous to the v-
TITLE: myc oncogene of avian myelocytomatosis virus
TITLE: MC29
JOURNAL: Nature
VOLUME: 301
PAGES: 722-725
DATE: 1983
AUTHORS: Saito, H, Hayday, A C, Wiman, K G,
AUTHORS: Hayward, W S, Tonegawa, S.
TITLE: Activation of the c-myc gene
TITLE: by translocation: a model for translational
TITLE: control
JOURNAL: Proceedings of the National Academy of
JOURNAL: Sciences, USA
VOLUME: 80
PAGES: 7476-7480
DATE: 1983
AUTHORS: Gazin, C, Rigoley, M, Briand, J P, Van
AUTHORS: Regemortel, M H V, Galibert, F.
TITLE: Immunochemical detection of
TITLE: proteins related to the human c-myc exon 1
JOURNAL: EMBO Journal
VOLUME: 5
PAGES: 2241-2250
DATE: 1986
RELEVANT RESIDUES IN SEQ ID NO: 11 :FROM 1 TO 18
US-08-173-489C-11

Query Match 0.7%; Score 14; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 gaagatgaggaaga 24
|||||
Db 3 GAAGATGAGGAAGA 16

RESULT 34

US-08-417-210A-52/c
; Sequence 52, Application US/08417210A
; Patent No. 5863542
; GENERAL INFORMATION:
; APPLICANT: PAOLETTI, ENZO
; APPLICANT: TARTAGLIA, JAMES
; APPLICANT: COX, WILLIAM I.
; TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXVIRUS
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
; STREET: 530 FIFTH AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,210A
; FILING DATE: 05-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KOWALSKI, THOMAS J.
; REGISTRATION NUMBER: 32,147
; REFERENCE/DOCKET NUMBER: 454310-2690
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-840-3333
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-417-210A-52

Query Match 0.7%; Score 14; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 gatgaagacgatga 69
|||||
Db 14 GATGAAGACGATGA 1

RESULT 35

US-08-585-684B-2737/c
; Sequence 2737, Application US/08585684B
; Patent No. 5877021
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: Jarvis, Thale
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: INDUCTION OF GRAFT TOLERANCE
; TITLE OF INVENTION: AND REVERSAL OF IMMUNE RESPONSES
; NUMBER OF SEQUENCES: 2751
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street

; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/585,684B
; FILING DATE: January 16, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/000,951
; FILING DATE: July 7, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 218/078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2737:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-585-684B-2737

Query Match 0.7%; Score 14; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1155 cagcaagcagccat 1168
|||||
Db 15 CAGCAAGCAGCCAT 2

Search completed: May 17, 2002, 18:18:30
Job time: 6691 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 17, 2002, 16:26:59 ; Search time 90.41 Seconds
(without alignments)
5474.522 Million cell updates/sec

Title: US-10-007-010-3
Perfect score: 2015
Sequence: 1 cggaggcaggaagatgagg.....atataatgcaagtcttacg 2015

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues
Word size : 0
Total number of hits satisfying chosen parameters: 615614

Minimum DB seq length: 0
Maximum DB seq length: 105

Post-processing: Listing first 65 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	18	0.9	20	US-08-910-629A-31
2	18	0.9	20	US-08-910-629A-42
3	18	0.9	20	US-09-209-568-7
4	18	0.9	20	US-09-287-796-31
5	18	0.9	20	US-09-287-796-42
6	18	0.9	20	US-09-130-616-31
7	18	0.9	20	US-09-130-616-42
8	17	0.8	20	US-08-730-876-2
9	17	0.8	20	US-09-430-692-71
10	17	0.8	23	US-08-222-616-2
11	17	0.8	23	PCT-US95-04228-2
12	16	0.8	24	US-08-859-998-598
13	16	0.8	24	US-09-225-928-598
14	15	0.7	18	US-08-951-923-51
15	15	0.7	18	US-08-584-040-6218
16	15	0.7	19	US-08-400-580A-11
17	15	0.7	31	US-08-942-423-51
18	15	0.7	36	US-08-951-923-52
19	15	0.7	36	US-08-724-586-3
20	15	0.7	36	US-09-421-632-3
21	15	0.7	45	US-08-039-198B-3
22	15	0.7	72	US-08-707-237A-47
23	15	0.7	104	US-09-058-389A-19
24	15	0.7	105	US-09-461-697-78
25	14	0.7	17	US-08-584-040-7661
26	14	0.7	18	US-08-105-483-197
27	14	0.7	18	US-08-220-151-78

Sequence 78, Appl	1	US-08-413-118-78	18	0.7	14	C 28
Sequence 54, Appl	1	US-08-224-657-54	18	0.7	14	C 29
Sequence 197, Appl	1	US-08-709-201-197	18	0.7	14	C 30
Sequence 197, Appl	1	US-08-458-101-197	18	0.7	14	C 31
Sequence 52, Appl	2	US-08-184-009-52	18	0.7	14	C 32
Sequence 11, Appl	2	US-08-173-489C-11	18	0.7	14	C 33
Sequence 52, Appl	2	US-08-417-210A-52	18	0.7	14	C 34
Sequence 2737, Ap	2	US-08-585-684B-2737	18	0.7	14	C 35
Sequence 52, Appl	2	US-08-458-356-52	18	0.7	14	C 36
Sequence 2737, Ap	2	US-08-473-446-78	18	0.7	14	C 37
Sequence 78, Appl	3	US-09-038-073-2737	18	0.7	14	C 38
Sequence 2737, Ap	4	US-08-460-736-52	18	0.7	14	C 39
Sequence 52, Appl	18	US-09-354-138-54	18	0.7	14	C 40
Sequence 6, Appl	20	US-08-639-763-6	20	0.7	14	C 41
Sequence 44, Appl	21	US-08-056-200-44	21	0.7	14	C 42
Sequence 44, Appl	21	US-08-800-644-44	21	0.7	14	C 43
Sequence 66, Appl	21	US-08-953-094-66	21	0.7	14	C 44
Sequence 2, Appl	22	US-07-955-916-2	22	0.7	14	C 45
Sequence 549, App	22	US-08-379-078-549	22	0.7	14	C 46
Sequence 172, App	22	US-07-974-409C-172	22	0.7	14	C 47
Sequence 172, App	22	PCT-US93-00977-172	22	0.7	14	C 48
Sequence 17, Appl	24	US-07-842-349-17	24	0.7	14	C 49
Sequence 39, Appl	24	US-08-151-574-39	24	0.7	14	C 50
Sequence 39, Appl	24	US-08-391-000-39	24	0.7	14	C 51
Sequence 15, Appl	24	US-08-480-994-15	24	0.7	14	C 52
Sequence 15, Appl	24	US-08-616-844-15	24	0.7	14	C 53
Sequence 39, Appl	24	US-08-419-448-39	24	0.7	14	C 54
Sequence 39, Appl	24	US-07-952-853-8	24	0.7	14	C 55
Sequence 39, Appl	24	US-08-741-931-39	24	0.7	14	C 56
Sequence 15, Appl	24	US-08-599-654-15	24	0.7	14	C 57
Sequence 15, Appl	24	US-08-485-573-15	24	0.7	14	C 58
Sequence 8, Appl	24	US-08-914-848-8	24	0.7	14	C 59
Sequence 15, Appl	24	US-08-944-868A-15	24	0.7	14	C 60
Sequence 15, Appl	24	US-08-944-423A-15	24	0.7	14	C 61
Sequence 15, Appl	24	US-08-925-743-15	24	0.7	14	C 62
Sequence 15, Appl	24	US-08-944-496-15	24	0.7	14	C 63
Sequence 15, Appl	24	US-08-925-767-15	24	0.7	14	C 64
Sequence 39, Appl	24	US-09-233-510-39	24	0.7	14	C 65

ALIGNMENTS

RESULT 1
US-08-910-629A-31/c
; Sequence 31, Application US/08910629A
; Patent No. 5877309
; GENERAL INFORMATION:
; APPLICANT: Robert A. McKay
; APPLICANT: Nicholas M. Dean
; APPLICANT: Brett Monia
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF JNK
; TITLE OF INVENTION: PROTEINS
; NUMBER OF INVENTIONS: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
; MEDIUM TYPE: STORAGE
; COMPUTER: PENTIUM
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,629A
; FILING DATE: August 13, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0215
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: Yes
US-08-910-629A-31

Query Match 0.9%; Score 18; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 gactttggcctggccgg 1317
|||||
Db 20 GACTTTGGCCTGGCCGG 3

RESULT 2
US-08-910-629A-42
Sequence 42, Application US/08910629A
Patent No. 5877309
GENERAL INFORMATION:
APPLICANT: Robert A. McKay
APPLICANT: Nicholas M. Dean
APPLICANT: Brett Monia
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF JNK
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
CITY: Marlton
STATE: NJ
COUNTRY: USA
ZIP: 08053
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
MEDIUM TYPE: STORAGE
COMPUTER: PENTUM
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,629A
FILING DATE: August 13, 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0215
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 779-8488
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear

ANTI-SENSE: NO
US-08-910-629A-42

Query Match 0.9%; Score 18; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 gactttggcctggccgg 1317
|||||
Db 1 GACTTTGGCCTGGCCGG 18

RESULT 3
US-09-209-668-7/C
Sequence 7, Application US/09209668A
Patent No. 6114517
GENERAL INFORMATION:
APPLICANT: Monia, Brett P.
APPLICANT: Xu, Xiaoxing S.
TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
FILE REFERENCE: ISPH-0336
CURRENT APPLICATION NUMBER: US/09/209,668A
CURRENT FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antisense sequence
US-09-209-668-7

Query Match 0.9%; Score 18; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 gactttggcctggccgg 1317
|||||
Db 20 GACTTTGGCCTGGCCGG 3

RESULT 4
US-09-287-796-31/C
Sequence 31, Application US/09287796A
Patent No. 6133246
GENERAL INFORMATION:
APPLICANT: McKay, Robert A.
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett
APPLICANT: Nero, Pam
APPLICANT: Gaarde, William A.
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS
FILE REFERENCE: ISPH-0350
CURRENT APPLICATION NUMBER: US/09/287,796A
CURRENT FILING DATE: 1999-04-07
EARLIER APPLICATION NUMBER: 09/130,616
EARLIER FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 08/910,629
EARLIER FILING DATE: 1997-08-03
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 31
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-287-796-31

KW polymerase chain reaction; ss.

XX Synthetic.

PN W09514772-A1.

XX W01-JUN-1995.

XX 11-NOV-1994; 94WO-JP01916.

XX 12-NOV-1993; 93JP-0355504.

XX (MATSU) MATSUBARA K.

PA (OKUBO/) OKUBO K.

XX Matsubara K, Okubo K;

XX WPI; 1995-206931/27.

XX Identifying gene signatures in 3'-directed human cDNA library - e.g.

PT for diagnosis of abnormal cell function, by preparing cDNA that

PT reflects relative abundance of corresp. mRNA in specific human

PT tissues

XX Example 7; Fig 8; 2245pp; Japanese.

XX Primers T41001-T41782 are derived from novel human gene signature (GS)

CC sequences which did not match with sequences deposited in Genbank release

CC 76. The GS sequences (T19001-T36837) were obtained from 3'-directed cDNA

CC libraries prepared from various human tissues; synthesis of cDNA was

CC initiated from the 3'-end of mRNA by using poly(T) as the sole primer.

CC Each library is constructed so as to reflect accurately the relative

CC abundance of different mRNAs in the particular tissue from which it was

CC derived. The appearance frequency of a given GS in a cDNA library can be

CC determined (esp. using primers and probes derived from the GS sequences)

CC as a means of diagnosing abnormal cell function or for recognising

CC different cell types. The primers T41207-8 amplify clone pm0112 which

CC comprises the GS HUMGS001089 (T20089), located on chromosome 20.

XX Sequence 20 BP; 2 A; 6 C; 4 G; 8 T; 0 other;

Query Match 1.0%; Score 20; DB 16; Length 20;

Best Local Similarity 100.0%; Pred. No. 19;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1673 aacagcagccatgataggga 1692

Db 20 AACAGCAGCCATGATAGGGA 1

RESULT 22

AAL33024/c

ID AAL33024 standard; DNA; 51 BP.

XX AC

XX AAL33024;

XX 24-JAN-2002 (first entry)

XX Human SNP oligonucleotide #6232.

XX Immunosuppressive; immunostimulatory; antinflammatory; cytostatic;

XX neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;

XX amyloid protein; angiotensin; apoptosis related protein; cadherin;

XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;

XX complement related protein; cytochrome; kinesin; cytokine; interferon;

XX interleukin; G-protein coupled receptor; thioesterase; inflammation;

XX multifactorial disease; autoimmune disease; infection;

XX nervous system disease; ss.

XX Homo sapiens.

XX W0200147944-A2.

XX PD

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

05-JUL-2001.

28-DEC-2000; 2000WO-US35498.

28-DEC-1999; 99US-0173419.

27-DEC-2000; 2000US-0173419.

(CURA-) CURAGEN CORP.

Shimkets RA, Leach M;

WPI; 2001-465210/50.

Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,

oncogenes and histones, useful for diagnosing and treating, e.g.

cancer, autoimmune diseases and infections -

Claim 1; Page 3170; 4143pp; English.

The present invention relates to oligonucleotides encoding polymorphic

variants of proteins related to amylases, amyloid proteins, angiotensin,

apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,

histones, kinases, colony stimulating factors, complement related

proteins, cytochromes, kinesins, cytokines, interferons, interleukins,

G-protein coupled receptors and thioesterases. The present sequence is

one such oligonucleotide. The oligonucleotides and the peptides encode;

diseases associated with inappropriate expression of the proteins listed

above. Disorders that may be prevented, diagnosed and/or treated include

multifactorial diseases with a genetic component, such as autoimmune

diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,

systemic lupus erythematosus and Grave's disease), inflammation, cancer

(e.g. cancers of the bladder, brain, breast, colon and kidney,

leukaemia), diseases of the nervous system and an infection of pathogenic

organisms.

Sequence 51 BP; 7 A; 14 C; 19 G; 11 T; 0 other;

Query Match 0.9%; Score 19; DB 22; Length 51;

Best Local Similarity 100.0%; Pred. No. 61;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1232 actacatccaccgagacct 1250

Db 25 ACTACATCCACCAGACCT 7

RESULT 23

AAL33025/c

ID AAL33025 standard; DNA; 51 BP.

XX AC

XX AAL33025;

XX 24-JAN-2002 (first entry)

XX Human SNP oligonucleotide #6233.

XX Immunosuppressive; immunostimulatory; antinflammatory; cytostatic;

XX neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;

XX amyloid protein; angiotensin; apoptosis related protein; cadherin;

XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;

XX complement related protein; cytochrome; kinesin; cytokine; interferon;

XX interleukin; G-protein coupled receptor; thioesterase; inflammation;

XX multifactorial disease; autoimmune disease; infection;

XX nervous system disease; ss.

XX Homo sapiens.

XX W0200147944-A2.

XX PD

05-JUL-2001.

